b-17.rpr

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OM protein - protein search, using sw model

December 4, 2003, 19:48:34; Search time 20 Seconds (without alignments) 1211.725 Million cell updates/sec Run on:

Title: Perfect score:

US-09-857-826B-17 1348 1 MAELEFVQIIIIVVVMMVMV......PLESAAIWSKEKDKQKGHPL 252 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description					١	atrophin-1 - human	hypothetical prote	tastin - human	tumor suppressor p	class VII unconven				æ	hypothetical prote			hypothetical prote		hypothetical 69K p	rotei	U	hypothetical prote			_	_	_	_
SUMMARIES	a	T00388	T09046	T48627	S19150	G01763	S50832	C84534	I38487	A56155	A59249	T33606	\$01955	T29265	851796	T28734	T00062	T06291	T16755	S00256	JQ0110	T49403	T01456	\$33015	T06076	T43456	T51904	492	ın	T00065
	Length DB							727 2				1145 2						760 2									1051 2			1172 2
do	Query Match Le	9.3	9.5	9.1	8.4	8.3	8.3	8.2	8.2	8.1	7.9	7.8	7.6	7.6	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.3
	Score	125.5	123.5	122	113	111.5	111.5	111	110.5	109.5	101	105	103	102.5	101	101	101	100.5	100	100	100	100	99.5	99.5	66	66	66	98.5	98	98
	Result No.	н	7	е	4	ហ	9	7	60	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote hydroxymroline-ric	hypothetical prote 99.7K hypothetical immediate early pr	genome polyprotein PTB-associated spl hymothetical prote	insulin receptor s proline-rich pepti protein-tyrosine k	cytokine receptor extensin-like prot	salivary proline-r extensin precursor
.B70700 T15331	D96728 C86371 EDBEIF	RRWPTM A46302 T30930	JC5209 A41819 A49508	A35782 T47617	PIHUSD S25299
000	1001	- 7 C	000	7 7	7
527 436	710 895 1460	1844 707 998	1240 5762 876	896 951	310
7.2	7.1.7	7.1	7.1	7.0	7.0
97	9 9 9	95.5	9 9 9 9 0 0 1 0 0 1 0 0 1 0 0	95 95	94.5 94.5
31	1 W W W 1 W 4 W	36 37 86	0 6 4 4 0 0 0 1	4 4 3	4 4 7 4

## ALIGNMENTS

RESULT 1 T00388

hypotl	hypothetical protein KIAA0616 - human (fragment)
C, Spe	C.Species: Homo sapiens (man) C.natol-Ot-Bahiloso Hacmience revision 01-Pah-1999 Hiext change 21-Jul-2000
C; Acc.	C;Accession: T00388
R; Ish.	R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
V DNA R	DNA Res. 5, 169-176, 1998
A;Tit.	A, Title: Prediction of the coding dequences of unidentified human genes. X. The complete
A; Ret	A;kererence number: <u>Z14142; Mer</u> D:98403880; PMID:9734811 A:Accessi <del>on: 1703</del> 88
A; Stal	A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mol	A; Molecule type: mRNA
A;Res:	A;Residues: 1-634 <ish></ish>
A; Cro	A;Cross-references: EMBL:AB014516; NID:g3327045; PIDN:BAA31591.1; PID:g3327046
A; Exp	A;Experimental source: brain
A;Gen	A;Gene: KIAA0616
6	Mistry Match 0 3%. Grove 195 6. DR 2. Length 634.
A C	Similarity
Mati	Matches 53; Conservative 24; Mismatches 63; Indels 75; Gaps 8;
ò	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
qq	:   :   :
ò	81 TDRLAVPPRAGRERFHREGPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTL 132

., 8 374 -----PPASQQ------PPPPPPPAPPRLPPGGPLLPSASLTRGPQPPPLAVTVPSSL 421 133 QLRDPEQ------QLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSG 178 ----- PTSPVSNQG 467 422 PQSPPENPGQPSMGIDIASAPALQQYRTSAGSPANQS-----179 ISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQ 213 | : : | : | | FS------PGSSPQHTSTLGSVFGDAYYEQQ 492 468 유 ઠે g ò 원 proline-rich protein F26K10.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Unn-1999 #sequence\_revision 11-Jun-1999 #text\_change 22-Oct-1999
C;Accession: T09046
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro submitted to the Protein Sequence Database, June 1999
A;Reference number: 216533
A;Accession: T09046
A;Molecule type: DNA
A;Residues: 1-508 <BEV>

1

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92 RERFHRFQPTYPYLQHEI-
                                                                                                                                                                                                                                                                                                                                                              63; Conservative
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Best Local Similarity
Matches 48; Conserv
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CiDate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
CiDate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
CiAccession: T48627
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Is submitted to the Protein Sequence Database, April 2000
A;Reference number: 224493
A;Recession: T48627
A;Retus: preliminary
A;Molecule type: DNA
A;Retus: preliminary
A;Rotaus: Dreliminary
A;Rotaus: DNA

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                                                                                                                                                                                                                                                                                                                                                                  70 PEPQVYAPPRPTDRLAVPP-----FAQRERFHRFQPTYP----YLQHEIDLPPTISLS 118
                                                                                                                                                                                                                                                                                                                                                                                                                               271 PPSÓLQAPPAQSQFMPPPPAPSHPSSAÓTQSFPQYQQNWPPQPQARPQSSGGYPTYSPAP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 PGNQPPVESLPSSMQMQSPYSGP------PQQSMQAYGYGAAPPPQAPPQQTKMSYSPQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 TGDGYLPSGPPP---SGYANAMY-EGGRMQYPPPQPQQQQQQAHYLQGPQGGGYSPQPH 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 SGNGIPEPQV---YAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 NPEEPPY------PQQSYPPN--PPRQPPSHPPPGSAPSQQYYNAPPTPPSMYDGP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 SGGSQPPPTIQPPYQPPPTQSLHQPPYQPPPQ----QPQYPQ----QPPPQLQHPSGY
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 LG-----GPCPPSSNSGISATCYGSGGRMEGPP--PTYSEVIGHY-----PGSSFQHQ
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                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                  Length 508;
Cross-references: EMBL:AL049803; GSPDB:GN00062; ATSP:F26K10.180; Experimental source: cultivar Columbia; BAC clone F26K10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%; Score 122; DB 2; Length 530;
29.1%; Pred. No. 0.041;
tive 8; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                              Query Match 9.2%; Score 123.5; DB 2; Best Local Similarity 26.4%; Pred. No. 0.03; Matches 51; Conservative 18; Mismatches 71;
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Best Local Similarity 29.1:
Matches 48; Conservative
                                                                                           A;Gene: ATSP:F26K10.180
A;Map position: 4
A;Introns: 52/3; 160/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
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                                                                   Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 D-----RESVRAPPNRTIFDSDLMD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 DLGRIPGFPIPPKIPIRIPESRIIASPIDIAPLDSDPVLSVRTEVHAPERRIFMDPEALR 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPTISLSDGEEPPPYOGPCTLOLRDPEQQLELNRESV--RAPPNRTIFDSDLMDSARLGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 PPPTŚLŚVSNOPPKYTOP-----SLPSQAVWSQGPPPPPPYGRLLANSNAHPG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCPPSSNSGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQQ-----SSGP---- 217
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A;Accession: S19150
A;Status: preliminary
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Coss-references: EMBL:X16378; NID:g62218; PIDN:CAA34414.1; PID:g62219
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Homo sapiens (man)
C.Species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C.Accession: G01763
R.Margolis, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLPPTISLSDGEEPPPYQGPC----TLQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 HRRSYPFLPNPPAALPSIAYTSSRGKIHHSLPKGALPKEGAPPPRRLPSPAPHPQLPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 SARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFOHQQSSGPPSLLEG
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                                                                                                                                                                                                                                                                                                                                                  47 REDALSSEG-----CL-WPSESTVSGNGIPE----PQVYAP---PRPTDRLAVPPFAQ
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                                                                                                                                                                                                                                                                                               96;
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                                                                                                                                                                                                                                          Length 628;
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A;Cross-references: EMBL:U23851; NID:g915325; PID:g915326
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                                                                                                                                                                                                                                                                                               92;
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                                                                                                                                                                                                                                          8.4%; Score 113; DB 2;
24.0%; Pred. No. 0.25;
tive 21; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Score 111.5; DB 24.7%; Pred. No. 0.68; ative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1995
A, Reference number: G08343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Gene: GDB:DRPLA; B37
A;Cross-references: GDB:270336; OMIM:125370
A;Map position: 12p-12p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 SSSAAASSSSSSSSSASPFPASQA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 TRLHHTHIAPLESAAIWSKEKD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 -PSLLEGTRLHHTH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPHPLEGGSSHHAH 522
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hypothetical protein, 69K - turnip yellow mosaic virus C;Species: turnip yellow mosaic virus, TYMV C;Date: 20-Peb-1995 #sequence\_revision 20-Peb-1995 #text\_change 17-Mar-2000 C;Accesion: S19150 R;Dreher, T.W.; Bransom, K.L. Plant Mol. Biol 18, 403-406, 1992 ო

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A; Accession: A56155
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                                                187
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Feb-2001
C;Accession: C84534
R;Lin, X.; Kaul
S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-727 cSTO>
A;Cross-references: GB:AE002093; NID:g5306245; PIDN:AAD41978.1; GSPDB:GN00139
C;Genetics:
A;Gene: Ar2g15880
A;Map position: 2
                                                                                    C;Species: Homo sapiens (man)
C;Date: 14-Uul-1995 #sequence_revision 21-Jul-1995 #text_change 07-May-1999
C;Accession: S50832
R;Nagafuchi, S:; Yanagisawa, H.; Ohsaki, E.; Shirayama, T.; Tadokoro, K.; Inoue, T.; Yam
Nature Genet. 8, 177-181, 1994
                                                                                                                                                                                                             A;Title: Structure and expression of the gene responsible for the triplet repeat disorde A;Reference number: S50832; MUID:95144175; PMID:7842016 A;Actersion: S50832 A;Actersion: S50832 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LPSYPH----SF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESV--RAPPNRTIFDSDLMDSARLGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 PPPTSLSVSNQPPKYTQP-----SLPSQAVWSQGPPPPPPYGRLLANSNAHPG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQ-----SSGP---- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 РЕРРЗ------ТGAQSTAHPPVSTHНННООООООООООООННGNSGPPPGA 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 PEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1184;
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25.0%; Pred. No. 0.43;
.ive 18; Mismatches 54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.3%; Score 111.5; DB 2;
Best Local Similarity 24.7%; Pred. No. 0.68;
Matches 48; Conservative 14; Mismatches 67;
                                                                                                                                                                                                                                                                                     A Status: preliminary
A Molecule type: mRNA
A;Residues: 1-1184 «NAG>
A;Cross-references: EMBL:D31840
C;Genetics: A;Genetics: A;Genetics: A;Genetics: CDB:DRPLA; B37
A;Gene: GDB:DRPLA; B37
A;Genetics: CDB:270336; OMIM:125370
A;Map position: 12p13.31-12p13.3112p-12p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 SSSAAASSSSSSSSSASPPASQA---
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Matches 40; Conserv
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C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C;Accession: 138487
C;Accession: 138487
R;Fukuda, M.N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami, M.; Aoki, D.; Nozawa, S.
Genes Dev. 9, 1199-1210, 1995
A;Title: Trophinhin and tastin, a novel cell adhesion molecule complex with potential inv
A;Reference number: 138487; MUID:95278733; PMID:7758945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: FlyBase:FBgn0011739
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C;Keywords: ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Drosophila melanogaster
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
C;Accession: A56155
R;Justice, R.W; Zilian, O; Woods, D.F.; Noll, M.; Bryant, P.J.
Genes Dev. 9, 534-546, 1995
A;Title: The Drosophila tumor suppressor gene warts encodes a homolog of human myotonic A;Reference number: A56155; MUID:95212904; PMID:7698644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor suppressor protein warts (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)
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   -----PPKMSSPPTQTPVNSPPP 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 NGIP-----EPQVYAPPRPIDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NRTIFDSDLM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 PPA---EPRPLESCCRSEPEIPESSROEQLEVPEPCPPAEPRPLESYCRIEPEIPESSRO 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQ--QSSGPPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | | | | : : | : | | | | | | EQLEVPEPCPPAEPGPLOPSTOGOSG-PPGPCPRVE--LGASEPCTLEHRSLESSLPPCC 662
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A;Molecule type: mRNA
A;Residues: 1-1099 «JUS»
A;Cross_references: GB:L39837; NID:g755007; PIDN:AAA73959.1; PID:g755008
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                                                                                                         : | | | | : : | | STPSQTVEAPPPSEFIIPPFIG----HQYASPPPMFQG 726
                                                                ---GGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEG
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26.6%; Pred. No. 0.9;
ative 18; Mismatches 80;
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Pred. No. 0.51;
648 PPVYSPPP-----PPVKSPPPPVYSPPLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
8.2%; Score 110.5; Best Local Similarity 24.5%; Pred. No. 0.51
Matches 52; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-778 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Dictyostelium discoideum
Cispecies: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
Cispecies: M.A.; Kuspa, A.; Loomis, W.F.
Proc. Natl. Acas Sci. US.A. 91, 9446-9450, 1994
A;Titus, M.A.; Kuspa, A.; Loomis, W.F.
A;Accession: A59249
A;Accession: A59249
A;Accession: A59249
A;Accession: A59249
A;Residues: DNAY; not compared with conceptual translation
A;Molecule type: DNAY; not compared with conceptual translation
A;Molecule type: DNAY; not compared with conceptual translation
A;Residues: 1-2357 <ATT>
A;Accession: A;Access
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Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
Cipate: 73-Accession: 73-866
Air Description: The sequence of C. elegans cosmid F54C4.
Air Reference number: Z21376
Air Reference n
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                                                                                                                                                                                                                                                                                                                                                                129 PCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGG 188
SHYLRCSPALDS--GAGSSRSDSPHSHHTHQPSSRTVGNPGGNGGFSPSPSGFSEVAPPA 197
                                                                                                  ----DLPPTISLSDGEEPPP 125
                                                                                                                                                                                                                                                                                                  126 YQG--PCTLQ--LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F54C4.3 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                          -----PPVPPTSQAYVKRRSPALNNRPPAIA-----PPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 ---GAĞGAAPPPPPPSYTASMQSRQSPTQSQQSDYRKSPSSGIYSATSAĞSPS 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PTYSEVIGH--YPGSSFOHOOSSGPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMMGIPPPPPTISV-----HSLSNSGNSTPP 1793
                                                                                             PTDR-----LAVPPFAQRERFHRFQPTYPYLQHEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: myol
C,Superfamily: myosin motor domain homology
F,16-676/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 RMEG---PPPTYSEVIGHYPGSSFQHQOSSGPP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.9%; Score 107; DB Best Local Similarity 28.1%; Pred. No. 3.3; Matches 43; Conservative 12; Mismatches
                                                                                                                                                                                          198 PPPRNPTASSAATPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1725 ----MLPPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TCYGSGGRMEGPP-
                                                                                                  80
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A;Gene: CESP:F54C4.3
Map position: 3. Map position: 264/3; 307/3; 357/2; 371/2; 432/1; 515/3; 564/2; 63
A;Introns: 57/3; 98/1; 167/3; 193/1; 264/3; 307/3; 357/2; 371/2; 432/1; 515/3; 564/2; 63
C;Superfamily: Caenorhabditis elegans hypothetical protein F54C4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: turnip yellow mosaic virus
C.Species: turnip yellow mosaic virus
C.Species: turnip yellow mosaic virus, TYMV
C.Accession: S01955
R.Morch, M.D.; Boyer, J.C.; Haenni, A.L.
Nucleic Acids Res. 16, 6157-6173, 1988
A.Title: Overlapping open reading frames revealed by complete nucleotide sequencing of A.Reference number: S01955; MulD:88289359; PMID:3399388
A.Status: preliminary
A.Status: preliminary
A.Status: 1-628 <AMOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           970 QESVLPPPPRETTRSVVRSRKRRDRFAELRDCPPEVMRAİAAHAIAYDGRKKEQRPIVY 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1030 VPRQAKMAMSSTPTAPTPPEDYDGPPGHQMTTILQHQRQAKQEEEEEQWSGEYDDELHEQ 1089
                                                                                                                                                                                                                                                                                                                                                             -----RESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PQT 536
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C;Species: Caenorhabditis elegans
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T2265
                                                                                                                                                                                                                                                                                                                         86 VPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQL-ELN
                                                                                                                                                                                                                                                                                                                                                                                                                                           145 RESVRAPPNRTIFDSDLMDSARLGG-----PCPPSSNSGISATCYGSGGRME----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.)Cross-references: EMBL:X07441; NID:g62222; PIDN:CAA30321.1; PID:g62223 A;Note: the authors translated the codon ACG for residue 459 as U C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                    84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHDPATSSPPPSLLPHTGPSEIVHREEEVHMMLPEEADLMDDDDQQ 1136
                                                                                                                                                                                                        7.8%; Score 105; DB 2; Length 1145; 21.6%; Pred. No. 2.1; tive 25; Mismatches 69; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SSGPPSLLEGTR----LHH---THIAPLESAAIWSKEKDKQ 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 DSDPVLSVRTEVHAPERRTFMDPEALRSALASLPSPPRS-VGIIHTA----
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A; Experimental source: strain Bristol N2; clone F54C4 C; Genetics:
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25.3%; Pred. No. 1.6;
ative 19; Mismatches 80;
                                                                                                                                                                                                     Query Match
Best Local Similarity 21.6*
Matches 49; Conservative
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Best Local Similarity
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R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, November 1996
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid CO1G8.
A;Reference number: Z20597
A;Accession: T29265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Molecule type: DMA
A;Molecule type: DMA
A;Residues: 1-1357 * DUZ>
A;Coss-references: EMBL:U80439; PIDN:AAB37645.1; GSPDB:GN00019; CESP:C01G8.7
A;Residues: 1-1357 * DUZ>
A;Coss-references: Exain Bristol N2; clone C01G8
C;Genetics: A;Gene: CESP:C01G8.7
A;Map position: 1
A;Map position: 1
A;Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------ORERFHRFQ-------PIYPYLQHEIDLPPTISLSDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PSESTVSGNGIPEPQV-----YAPP---RPTDRLAVPPFA------ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------APLESAAIWS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.6%; Score 102.5; DB 2; Best Local Similarity 21.1%; Pred. No. 4.1; Matches 60; Conservative 18; Mismatches 83;
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  17:50:00 2003
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223 GTRLHHTHIAPLESAAIWSKEKDKOKGH 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 4, 2003, 19:52:06 Job time : 22 secs
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C; Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C; Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C; Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C; Adcession: S:1796
A; Title: Molecular cloning, structural analysis and functional expression of the proline A; Reference number: S:1796; MUID:95129547; PMID:7828592
A; Accession: S:1796
A; Accession: C:1796
A; Accessi
                                                                                                                                                                                                                                                                                                                                             MPVVAPSTST-----QPTPTTGSYLANTLATPGPAHAPSSSMSHAHHVISQQQHQYPPGC 560
121 BEPPPYGGPCTLOLRDPEQOLELNRESVR----APPNRTIFDSDLMDSARLGGPCPPSSN 176
                                                                                                                   461 PPPPAQG-----APSPSGAAGSNGKQPRYGTPAPPSR------ASAPTPQPLSST 505
                                                                                                                                                                                                                                      SGISATCYGSGGRMEGPPPTYSEVI-----GHYPGSSFQH------QQSSGPPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 REDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQR-ERFHRFQPTYP-Y 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 KEDATOFAAAMASALEALEGGGPPPPPPAAP-PTWSVQNGPASEEVEQQKRQQPGPPEH 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOHEID-----LPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDLMDSARLGGPCPPS-SNSGISATCYGSGGRMEGPP----PTYSEVIGHYPGS---- 207
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vasodilator-stimulated phosphoprotein VASP - dog
C;Species: Canis lupus familiaris (dog)
C;Species: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-944 <SAM>
A;Residues: 1-944 <SAM>
A;Cross-references: EMBL:AF022974; PIDN:AAC48041.1; GSFDB:GN00023; CESP:F26G5.9
A;Experimental source: strain Bristol N2; clone F26G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ESTVSGNGIPEP-----QVYAP----PRPTD----RLAVPPFAQRERFHRFQPTYPY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 LOHEID-LPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 QQQDLPFLPP------PPPHQ----LVMPPP-----AMPPPQH------MQ 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 SARL-GGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 AQRLWGGPQPQRMNQPMMAQV---GGR----PGQY--IMGHPP--PMHHQMQGGPPRNMY 477
                                                                                                                                                                                                                                                                           Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 101; DB 2; Length 944; Best Local Similarity 27.9%; Pred. No. 3.5; Matches 58; Conservative 16; Mismatches 66; Indels 6
                                                                                                                                                                                                                                                                        C'Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
C;Accession: T28734
R;Sammons, L.; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F26GS.
                                                                                                                                                                                                                                           hypothetical protein F26G5.9 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclication: CESP:F26GS.9
A,Rap position: 5
A,Introns: 12/3; 48/3; 258/3; 327/3; 643/1; 916/2
                                                    232 AIAGAKLRKVSKQEEASGGPPVPKAESTR 260
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version 5.1.6
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GenCore
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OM protein - protein search, using sw model

December Run on:

4, 2003, 19:49:24; Search time 21 Seconds (without alignments) 507.730 Million cell updates/sec

US-09-857-826B-17 1348 1 MAELEFVQIIIIVVVMMVMV......PLESAAIWSKEKDKQKGHPL 252

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 segs, 42310858 residues Searched:

Total number of hits satisfying chosen parameters:

328717

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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/cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\* Issued Patents .. .. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Appli	Appl.	2, Appl	Appli	Appli	18, Appl	I, Appl	Appli	Appli	Appli	Appli	Appli	Appli	•	, Appli	Appli	31455, A	1917, A	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli
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SUMMARIES	. QI	US-09-769-482-3	US-09-769-482-11	US-09-769-482-12	US-09-091-952A-3	US-09-091-952A-4	99-266	9-041-886-2	US-08-317-522A-5	US-08-439-818A-5	US-08-751-965-5	US-08-738-975-5	US-08-728-626-5	US-08-808-599A-5	US-09-233-857-13	US-09-442-100-2	US-08-939-106-2	31	US-09-252-991A-24917	US-08-396-479B-6	0	US-09-189-035-1	US-09-382-086-1	US-08-701-240-4	US-09-138-236-4	US-08-395-580-2	PCT-US95-02792-2	US-08-557-139-2
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	Score	1348	1332	845.5	842.5	791.5	111.5	111.5	110.5	110.5	110.5	110.5	110.5	110.5	109.5	109.5			σ		97.5		96.5	96.5	96.5	95.5	95.5	95.5
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Gaps

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9 9 ESTVSGNGI PEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 120 61 ESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 120 EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180

61

121

1 MAELEFVQIIIIVVVVMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS

1 MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS

100.0%; Score 1348; DB 4; Length 252; 100.0%; Pred. No. 1.4e-118; ive 0; Mismatches 0; Indels 0.

Best Local Similarity 100. Matches 252; Conservative

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Query Match

180

241 SKEKDKQKGHPL 252

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241 SKEKDKOKGHPL 252

e 4, Appl:	4	e 4, Appl:	4	~	e 1, Appli	17	16,	16,	9	28	e 1, Appli	H	280	e 17793, 1	19,	19,	e 19, Appl	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	
US-08-445-640-4	US-08-170-558-4	US-08-447-314-4	US-08-445-461-4	US-08-336-343A-2	US-09-508-691-1	US-09-087-134-11	US-09-121-321-16	US-08-933-803A-16	US-09-150-460B-6	US-09-252-991A-28446	US-08-522-726B-1	US-09-337-384-1	US-09-252-991A-28065	US-09-252-991A-17793	US-09-113-309-19	US-09-521-109-19	US-09-562-332-19	
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913	913	913	913	919	1242	534	671	671	1290	176	1495	1495	522	556	518	518	518	
7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.8	
94.5	94.5	94.5	94.5	94.5	94.5	93.5	93.5	93.5	93.5	93	93	93	92.5	92.5	92	92	92	
28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

	RESULT 1 US-09-769-482-3
	; Sequence 3, Application US/09769482 C PUT
	GENERAL INFORMATION:
	; APPLICANT: SRIVASTAVA, SHIV
	; APPLICANT: MOUL, JUDD W.
	; APPLICANT: XU, LINDA L.
	; APPLICANT: SEGAWA, TAKEHIKO
	; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATE
	; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
	; FILE REFERENCE: 04995.0057-00000
	; CURRENT APPLICATION NUMBER: US/09/769,482
	; CURRENT FILING DATE: 2001-01-26
	; PRIOR APPLICATION NUMBER: 60/178,772
	; PRIOR FILING DATE: 2000-01-28
_	; PRIOR APPLICATION NUMBER: 60/179,045
	; PRIOR FILING DATE: 2000-01-31
	, NUMBER OF SEQ ID NOS: 67
	; SOFTWARE: Patentin Ver. 2.1
	SEQ ID NO 3
	; LENGTH: 252
	; TYPE: PRT
	; ORGANISM: Homo sapiens
	US-09-769-482-3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3

US-09-769-482-12

i Sequence 12, Application US/09769482

i Patent No. 6566130

i GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: MOUL, JUDD W.

APPLICANT: SGAMA, TAKENTKO

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

FILE REFERENCE: 04995.0057-00000

CURRENT APPLICATION NUMBER: 60/179,769,482

CURRENT FILING DATE: 2001-01-26

PRIOR FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-26

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PATENTIN OF SEQ ID NOS: 67

SEQ ID NO 12
                                                                        GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
TAPLICANT: WULLINDA L.
APPLICANT: XV, LINDA L.
APPLICANT: XV, LINDA L.
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLECTIDE ARRAY
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT APPLICATION NUMBER: US/09/769,482
PRIOR APPLICATION NUMBER: 60/170,772
PRIOR FILING DATE: 2000-01-28
PRIOR PRILING DATE: 2000-01-28
PRIOR PLING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VET: 2:1
SEQ ID NO 11
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AELEFVQIIIIVVVVMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE
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98.8%; Score 1332; D
Best Local Similarity 100.0%; Pred. No. 4.2
Matches 249; Conservative 0; Mismatches
                                          Sequence 11, Application US/09769482
Patent No. 6566130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KEKDKOKGH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
RESULT 2
US-09-769-482-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-769-482-11
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118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 ASTCSSNGRMEGPPPTYSEVMGHHPGASFLHHQRS---NAHRGSRLQFQQ-NNAESTIVP 234
                                                                                                                                                                                                                            2 AELEFVQIIIIVVVMMVWVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE 61
                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                      1 AELEFAQIIIIVVVVTVMVVVIVCLLNHYKVSTRSFINRPNQSRREDGLPQEGCLWPSD
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compactible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 19-Apr-1999
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION:
                                                                                                                   Query Match 62.7%; Score 845.5; DB 4; Best Local Similarity 67.6%; Pred. No. 1.6e-71; Matches 169; Conservative 21; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-0CT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Detera-Wadleigh, Sevilla
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09091952A Patent No. 6458532 GENERAL INFORMATION:
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Yoshikawa, Takeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Esterling, Lisa E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanders, Alan R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 SKEKDKQKGH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||:: |:
235 IKGKDRKPGN 244
                  TYPE: PRT
CRGANISM: Homo sapiens
US-09-769-482-12
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LENGTH: 244
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62 STVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARL-GGPCPPSSNSGIS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 EPPPYGGPCTLQLRDFEQQMELNRESVRAPPNRTIFDSDLIDIAMYSGGPCPPSSNSGIS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 ASTCSSNGRMEGPPPTYSEVMGHHPGASFLHHQRS---NAHRGSRLQFQQ-NNAESTIVP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kingemore, Stephen
APPLICANT: Kingemore, Stephen
APPLICANT: Tchernev, Veliaar
TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak
TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-
TITLE OF INVENTION: Interacting Proteins
PILE REPERENCE: 1596-623
CURRENT APPLICATION NUMBER: US/09/266,225D
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.7%; Score 791.5; DB 4; Best Local Similarity 64.0%; Pred. No. 2.3e-66; Matches 160; Conservative 21; Mismatches 44;
                                                                                                                                           NAME: Smith, Timothy L. REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: 1...288
OTHER INFORMATION: Clone 22 isoform 2
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-0CT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 18, Application US/09266225D
; Patent No. 6573364
; GENERAL INFORMATION:
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                       LENGTH: 288 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternatively spliced
                                                                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nandabalan, Krishan
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SKEKDKOKGH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 IKGKDRKPGN 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SELEFAQIIIIVVVVTVMVVVIVCLINHYKVSTRSFINRPNOSRRREDGLPOEGCLWPSD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 EPPPYQGPCTLQLRDPEQQMELNRESVRAPPNRTIFDSDLIDIAMYSGGPCPPSSNSGIS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARL-GGPCPPSSNSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AELEFVQIIIIVVVMMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGE
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 306;
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TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
                                                                                                                                                                                                                                                                                                                                                           Query Match 62.5%; Score 842.5; DB 4; Length Best Local Similarity 67.2%; Pred. No. 4.1e-71; Matches 168; Conservative 22; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPEs Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERQ for Windows Version 2.0
                                                                                                                                                                                                                             LOCATION: 1...306
OTHER INFORMATION: Clone 22 isoform 1, unspliced protein sequence Description: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GERSHON, Billot S.
Baddner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09091952A
Patent No. 6458532
             TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
                                                                                          TYPE: amino acide
TYPE: amino acide
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
WOLECULE TYPE: protein
FEATURE:
(415) 576-0300
                                                                                                                                                                                                             mat_peptide
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295 IKGKDRKPGN 304
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                                                                                                                                                                                                           NAME/KEY:
TELEFAX:
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US-09-091-952A-4
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52 SSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDL 111
                                                                                                                                                                                                                         379 SSSAAAASSSSSSSSSSASPPASQA----SF 411
                                                                                                                                                                                                                                                                          112 PPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESV--RAPPNRTIFDSDLMDSARLGG 169
                                                                                                                                                                                                                                                                                                           170 PCPPSSNSGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQQ-----SSGP---- 217
                                                                                                                                                                                                                                                                                                                                                                                                                            460 PFPPS------TGAQSTAHPPVSTHHHHHQQQQQQQQQQHHGNSGPPPGA 508
                                                                                                                             65;
                                                                  DB 4; Length 1184;
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                                                                                                                             67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proaporotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
APPLICATION NUMBER: 13,815
FILING DATE:
CLASSIFICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
FEGISTRATION NUMBER: 31,815
FEGISTRATION NUMBER: 31,815
FEGISTRATION NUMBER: 619) 535-8949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids

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LENGTH: 1185 amino acids
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0.076;
67;
                                                                          Query Match 8.3%; Score 111.5; DB Best Local Similarity 24.7%; Pred. No. 0.076; Matches 48; Conservative 14; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09041886
Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 -PSLLEGTRLHHTH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 FPHPLEGGSSHHAH 522
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; ORGANISM: Homo sapiens
US-09-266-225D-18
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Matches 48; Conserv
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US-09-041-886-23
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52 SSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDL 111 SAAASSSSSSSSSSASPFPASQA----SF 412

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112 PPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESV--RAPPNRTIFDSDLMDSARLGG 169
                                           413 PPPTSLSVSNQPPKYTQP-----SLPSQAVWSQGPPPPPPYGRLLANSNAHPG 460
                                                                                                                                   461 РЕРЕЗ------ТĠAQSTAHPPVSTHHHHQQQQQQQQQQQQQHHGNSGPPPGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 NGIP------EPQVYAPPRPTDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 SLSDGEEPPPYQGPCTLQLRDPE----QQLELNRESVRAPP-----NRT1FDSDLM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 PPA---EPRPLESCCRSEPEIPESSROEOLEVPEPCPPAEPRPLESYCRIEPEIPESSRO 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 DSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQ--QSSGPPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 SGLPKPCLPEECGEPOPPAEPG----PP----EAFCKSEPEIPEPSLOEQLEVPEPY
                                                                                           PCPPSSNSGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQQ----SSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
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                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08317522A
Patent No. 5599918
GENERAL INFORMATION:
APPLICANT: FUkuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,522A
FILING DATE: 04-OCT-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   218 -PSLLEGTRLHHTH 230
                                                                                                                                                                                                                              510 FPHPLEGGSSHHAH 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-317-522A-5
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                                                                                        170
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FITLE OF INVENTION:
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                                                          ADDRESSEE:
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                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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US-08-738-975-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 NGIP-----EPQUYAPPRFTDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
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8.2%; Score 110.5; DB 1; Length 778;
Best Local Similarity 24.5%; Pred. No. 0.054;
Matches 52; Conservative 28; Mismatches 77; Indels 55
                                                                   Sequence 5, Application US/08439818A
Patent No. 5654145
GENERAL INFORMATION
APPLICANT: FURUDA, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-751-965-5

Sequence 5, Application US/08751965

Patent No. 5858360

GENERAL INFORMATION:

APPLICANT: Fukuda, Michiko N.

TITLE OF INVENTION: Trophinin and Trophinin-Assisting
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               663 -----SQWAPATTSLIFSSQ-----HPL 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERENCE/DOCKET NUMBER: P-LA 1563
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                             ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: (619) 535-901
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 778 Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-439-818A-5
                                                                                                                                                                                                                                                                 STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                             ADDRESSEE:
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67 NGIP------EPQVYAPPRPIDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 778;
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Patent No. 5880267
GENERAL INFORMATION:
APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,965
FILING DATE: Herewith
                                                                         E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Score 110.5; DB 2;
24.5%; Pred. No. 0.054;
ive 28; Mismatches 77;
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4370 La Jolla Village Drive, Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/439,818

FILING DATE: 12-MAY-1995

ATTORNEY, AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REGISTRATION NUMBER: P-LA 2252

TELECHONGUNICATION INFORMATION:

TELEPHONE: (619) 535-8949

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 778 amino acids

""""" amino acids
                                                                                                                                                                                                        ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 24.59
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-751-965-5
                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                            CITY: San Diego
STATE: California
COUNTRY: USA
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STATE: California
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67 NGIP-----EPQVYAPPRPTDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     606 EQLEVPEPCPPAEPGPLQPSTQGQSG-PPGPCPR--LGASEPCTLEHRSLESSLPPCC 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.2%; Score 110.5; DB 2; Length 778; Best Local Similarity 24.5%; Pred. No. 0.054; Matches 52; Conservative 28; Mismatches 77; Indels 55; Gaps
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US-08-808-599A-5
Sequence 5, Application US/08808599A
Sequence 5, Application US/08808599A
Sequence 5, Application US/0880859A
GENERAL INFORMATION:
APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin, Trophinin-Assisting
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,599A
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |: |: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .: || .
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                           APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1563
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (619) 535-9001
TELEPRAX: (619) 535-9001
TELEPRAX: (619) 535-9001
SECURATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 778 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-728-626-5
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 NGIP------EPQVYAPPRFTDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 SLSDGEEPPPYQGPCTLQLRDPE----QQLELNRESVRAPP------NRTIFDSDLM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 PPA---EPRPLESCCRSEPEIPESSRQEQLEVPEPCPPAEPRPLESYCRIEPEIPESSRQ 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 DSARLGGPCPPSSNSGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQ--QSSGPPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 EQLEVPEPCPPAEPGPLQPSTQGQSG-PPGPCPRVE--LGASEPCTLEHRSLESSLPPCC 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
8.2%; Score 110.5; DB 2; Length 778;
Best Local Similarity 24.5%; Pred. No. 0.054;
Matches 52; Conservative 28; Mismatches 77; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5. Application US/08728626
; Sequence 5. Application US/08728626
; Patent No. 5910451
; GENERAL INFORMATION:
    APPLICANT: Fukuda, Michiko N.
    TITLE OF INVENTION: Trophinin and Trophinin-Assisting; TITLE OF INVENTION: Proteins
    NUMBER OF SEQUENCES: 22
    CONFESSORENCE ADDRESS:
    ADDRESSEE: Campbell and Flores
    STREET: 4370 La Jolla Village Drive, Suite 700
    CITY: San Diego
    STATE: California
    COUNTRY: USA
                  MEDIUW TYPE: Floppy disk

COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,975
FILING DATE: Derewith
CLASSIFICATION NUMBER: US 08/439,818
FILING DATE: 05-Dec-1995
ATFORNEY/AGENT INPORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERRNCE/DOCKET NUMBER: 31,815
REFERRNCE/DOCKET NUMBER: 31,815
REFERRNCE/DOCKET NUMBER: 31,815
RELEPHAN: (619) 535-9001
TELEPHAN: (619) 535-9001
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LLEGTH: 777 8 main o acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92122

COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 PTDR-----LAVPPFAQRERFHRFQPTYPYLQHEI------DLPPTISLSDGEEPPP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 QRGNSPVITÓNGLKNÞQQQLTQQLKSLNLYÞGG-----GSGAVVEPPPPYLIQG--- 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TCYGSGGRMEGPP------PTYSEVIGH--YPGSSFQHQQSSGPPS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 109.5; DB 4; Length 1088; 26.6%; Pred. No. 0.11; tive 18; Mismatches 80; Indels 73;
                                                                                                                                                                                                                                                                                  Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                        116 SLSDGEEPPPYQGPCTLQLRDPE----QQLELNRESVRAPP---
                                                                                                                                                                                                                                                                              Query Match 8.2%; Score 110.5; DB 3; Best Local Similarity 24.5%; Pred. No. 0.054; Matches 52; Conservative 28; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09233857.

Patent No. 6495353
GENERAL INFORMATION
APPLICANT: Planagan, Gregory
APPLICANT: Flanagan, Peter
TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
FILE REFERENCE: 239,251
CURRENT APPLICATION NUMBER: US/09/233,857
CURRENT PILING DATE: 1999-01-20
GARLIER APPLICATION NUMBER: USSN 60/072,023
BARLIER PILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEPAX: (619) 535-9901
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 778 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.6
Matches 62; Conservative
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; MOLECULE TYPE: protein
US-08-808-599A-5
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US-09-233-857-13
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US-09-233-857-13
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290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 PTDR-----LAVPPFAQRERFHRFQPTYPYLQHEI------DLPPTISLSDGEEPPP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 YQG--PCTLQ--LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 SHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTV---SGNG--IPEPQVY---APPR
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182 TCYGSGGRMEGPP------PTYSEVIGH--YPGSSFQHQQSSGPPS 219
                                                                                                                             | Sequence 2, Application US/09442100
| Patent No. 6359193
| GENERAL INFORMATION:
| APPLICANT: Tao, Wafan
| APPLICANT: Tao, Wafan
| APPLICANT: Tao, Wang, Sheng
| APPLICANT: Tao, Wang, Sheng
| APPLICANT: Tao, Wang, Sheng
| TITLE OF INVENTION: WALL
| TITLE OF INVENTION: GENES AND METHODS BASED THEREON
| NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 109.5; DE; Pred. No. 0.11; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9900
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.6%;
Matches 62; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1099 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-442-100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                           RESULT 15
US-09-442-100-2
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Search completed: December 4, 2003, 19:52:39 Job time : 22 secs

us-09-857-826b-17.rai

# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 4, 2003, 19:44:54 ; Search time 18 Seconds (without alignments) 658.374 Million cell updates/sec

US-09-857-826B-17 1348 1 MAELEFVQIIIIVVVWMVWV.....PLESAAIWSKEKDKQKGHPL 252

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

ES	Description	шоц 6м6960	Q9d7r2 mus m		Q9nzm4 homo	Q91ka5 arabi	P28478 turn	P54259 homo	Q12815 homo	Q14162 homo	P10357 turn	P50551			075376	P03204 epste	Q8wxx7 homo	Ф 35246	Q14934 homo	. P13983 nicot	Q9c0c2	P20128	P23246 homo	Q12852	P26955 mus m	P10162	P34428	Q08345	P35568	P78621			09esd7	Ded 110050
SUMMARIES	ID	TMEP HUMAN	TWEP WOUSE	C181 HUMAN	GSR1 HUMAN	UMP1 ARATH	V70K TYMVC	DRPL HUMAN	TAST HUMAN	SREC HUMAN	V70K_TYMV	VASP_CANFA	DRPL RAT	V70K_TYMVA	NCR1_HUMAN	EBN6 EBV	AUT2_HUMAN	SHK1 HUMAN	NFC4 HUMAN	EXTN_TOBAC	TABP_HUMAN	POLR TYMVA	SFPQ_HUMAN	M3 KC_HUMAN	CYRB_MOUSE	PRPL_HUMAN	YL37 CAEEL	DDR1_HUMAN	IRS1 HUMAN	SEPA EMENI	Z282_HUMAN	DDR1_RAT	DYSF MOUSE	Vour BACCII
	DB	н	<del></del> 1	Н	H	-	М	<del>, -1</del>		H	H	H	~	<b>,-4</b>	Н	Н	H	~	~1	~	~	~	~	-	Н	Н	-	~	-	н	<del>, ,</del>	-	-	-
	* Query Match Length	287	260	306	1509	395	628	1185	778	830	628	384	1183	628	2440	992	1259	2161	905	620	1729	1844	707	829	896	276	466	913	1242	1790	671	910	2083	244
	Query Match	4.66	87.0	62.5	8.5	8.4	8.4	•	٠	7.7	7.6	7.5	7.5	7.4	7.4	7.4	7.3	•	7.2	7.1	٠	7.1	٠	٠	•	•	•	٠	•	•	٠	6.9	6.9	4
	Score	1340		842.5	114	113.5	113	111.5	110.5	104	103	101	100.5	100	100	99.5	98	ð	97.5	96	96	S.	95.5	95.5	95	94.5	94.5	94.5	94.5	94.5	93.5	93.5	93.5	6
	Result No.	-	7	ო	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	23

Ogmo81 arabidopsis Ogy618 h nuclear r P10161 homo sapien O54951 mus musculu Q09457 caenorhabdi Q92136 rattus norv Q9nr4 homo sapien P70056 kanopus lae O13508 penicillium Q9ury2 schizosacch P48434 gallus gall
S24B ARATH NCR2_HUMAN PREM HUMAN SM6B MOUSE YQ36_CAEEL TSC1. RAT RNC HUMAN WAS3_HUMAN WAS3_HUMAN ARRA PENRO ALP7_SCHPO SOX9_CHICK
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2517 2317 2317 2317 963 11163 1374 502 518 860 474
93 93 93 93 93 93 93 93 93 93 93 93 93 9
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# ALIGNMENTS

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                                                               Isold=Q969W9-2; Sequence=VSP 006438;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Highest expression in prostate. Also expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ^
        comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHRLMGVNSTAAAAGQPNVSCTCNCKRSLFQSMEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 1340; DB 1; Length 287; 99.2%; Pred. No. 9.7e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to membrane; NAS. receptor signaling pathway; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
WW-BINDING (POTENTIAL).
WW-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6103473561AE08DA CRC64;
                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                    -!- INDUCTIÓN: By androgen.
-!- SIMILARITY: BELONGS TO THE TMEPAI FAMILY.
                                                                                                                                                                                                                                                                                                                          IsoId=Q969W9-1; Sequence=Displayed;
                                      SEQUENCE OF 8-287 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL035541; CAB55862.1; -. EMBL; BC015918; AAH15918.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splicing
                                               TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF224278; AAF86322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 AA; 31609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016021; C:integral
GO; GO:0030521; P:androgen
Transmembrane; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL09357.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL16781.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:14107; TMEPAI.
        "The DNA sequence and con
Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
287
161
232
37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF305616;
                                                                                                                                                                                                                                                                                                                                                                              ovary.
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                                                                                                                                                                                                                                                                                                                  Name=1;
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DOMAIN
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Gaps

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Indels

1; Mismatches

Best Local Similarity 99.2 Matches 250; Conservative

Query Match

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collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Arawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Radawa T., Izawa M., Nishi K., Kiyosawa H., Konoo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Rakuhl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J., Rakuhl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bolinga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Raberich M., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Wanachi, V., Kawaji H., Kohtsuki S.,
                                                                                                                     ESTVSGNGIPEPQVYAPPRPTDRLAVPPPAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 155
                                                                                                                                                                                                            156 EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 215
                                                                                                                                                                                                                                                                              ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                                                                                                                                                                                                                      ALCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 275
9
                     36 ITELEFVOIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS 95
                                                                                          ESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG
                                                                                                                                                                                    EEPPPYOGPCTLOLRDPEQOLELNRESVRAPPNRT1FDSDLMDSARLGGPCPPSSNSG1S
MAELEFVQIIIIVVVMMVWVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20498735; PubMed=11042109; Jolliffe C.N., Harvey K.F., Haines B.P., Parasivam G., Kumar S.; "Identification of multiple proteins expressed in murine embryos as binding partners for the WW domains of the ubiquitin-protein ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane prostate androgen-induced protein (Nedd4 WW domain-binding protein 4).
TMEPAI OR N4WBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Interacts with the WW domains of NEDD4.
-!- SUBCELLULAR LOCATION: Type Ib membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE TMEPAI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ๙
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-Stomach;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0907R2; 09E0H9;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 351:557-565(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 59-260 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                           241 SKEKDKQKGHPL 252
                                                                                                                                                                                                                                                                                                                                                                                                                       276 SKEKDKOKGHPL 287
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the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                  ESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 120
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                                                                                                                                                                                                                                                                      1 MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS
                                                                                                                                                                                                                                                                                   18 ITELEFVQIVVIVVVVVVVVVVVVVITCLLSHYKLSARSFISRHSQARREDGLSSEGCLWPS
                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Brain;

TISSUB-Brain;

MEDLINE-981401214; PubMed=9479497;

YOSHIKRWA T., Sanders M.R., Esterling L.E., Detera-Wadleigh S.D.;

"Multiple transcriptional variants and RNA editing in C18orfl, a 1990e with LDLRA and transmembrane domains on 18p11.2.";

Genomics 47.246.257(198).

-I. SUBCELLULAR LOCATION: Type ID membrane protein (Potential).

-I. ALTERNATIVE PRODUCTS:

Event-Alternative splicipg; Named isoforms=4;

Name=Alpha-1;

ISOIGEO15165-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 260;
                                                               EMBL; AK008976; BAB26001.1; -.
EMBL; AF220208; AAG4247.1; -.
EMBL; AF220208; NawDy4.
GO; CO1015021; C:integral to membrane; ISS.
GO; GO:0005512; F:proceain binding activity; IPI.
GO; GO:0030521; P:androgen receptor signaling pathway; ISS.
                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                               WW-BINDING (POTENTIAL).
WW-BINDING (POTENTIAL).
31AD07BD16B0D77D CRC64;
                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                          87.0%; Score 1172.5; DB 1
88.1%; Pred. No. 3.2e-81;
:ive 11; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C181 HUMAN STANDARD; PRT; 306 AA. 015165; 015166; 015167; 015168; 16-007-2001 (Rel. 40, Created) C07-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=015165-2; Sequence=VSP_006440;
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43
260
139
210
28715 1
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Matches 222; Conservative
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                                                                                                                                                                   44 2
136 1
207 2
260 AA;
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C18ORFl.
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                                                                                                          GO; GO:002515
GO; GO:0030521
Transmembrane.
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                              194
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                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARL-GGPCPPSSNSGIS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 EPPPYQGPCTLQLRDPEQQMELNRESVRAPPNRTIFDSDLIDIAMYSGGPCPPSSNSGIS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
LDL-RECEPPOR CLASS A.
MPEAGFQATNAFECKFTCTSGKCIVLGSLVCNQQNDCGDN
SDEENCLLVTEHPPPGIFNS -> MAA (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AELEFVQIIIIVVVMMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-1 and isoform Beta-2).
/FTIdaVSP 006439.
Missing (in isoform Alpha-2 and
Beta-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R Genew, no....

R MIN 606571; -..

R GO, GO:0016021; Cintegral to membrane, ....

R InterPro; IPR002172; LDL_receptor_A.

B InterPro; IPR002172; LDL_receptor_A.

DR PAMRT; SM00192; LDLa, l. 1.

DR ROSITE; PS01209; LDLRA_1; FALSE_NEG.

DR PROSITE; PS50068; LDLRA_2; l. 1.

DR PROSITE; PS50068; LDLRA_2; l. 1.

DR PROSITE; PS50068; LDLRA_2; l. 1.

R POTENTIAL.

AS POTENTIAL.

AS POTENTIAL.
                                              Isold=015165-4; Sequence=VSP 006419, VSP 006440; SIMILARITY: BELONGS TO THE TMEPAI FAMILY. SIMILARITY: Contains 1 LDL-receptor class A domain.
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AA; 33900 MW; F48EF66E329201BD CRC64;
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(Rel. 40, Last sequence update)
IsoId=015165-3; Sequence=VSP_006439;
                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF009424; AAC52023.1; --
EMBL, AF009425; AAC52024.1; --
EMBL, AF009425; AAC52025.1; --
EMBL, AF00427; AAC52026.1; --
HSSP, P01130; 1AJJ.
Genew, HGNC:1224; C180xf1.
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Matches 168; Conservative
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295 IKGKDRKPGN 304
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ID GSR1 HUMAN
AC Q9NZM4;
DT 16-OCT-2001 (
DT 16-OCT-2001 (
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DOMAIN
VARSPLIC
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SEQUENCE FROM N.A.
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P28478;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                              brain,
                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                   Genomics 64:44-50(2000).
-!- TISSUE SPECIFICITY: Expressed at moderate levels in heart, brair
placenta, skeletal muscle, and pancreas, and at lower levels in
lung, liver, and kidney.
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 114; DB 1; Length 1509; (6.9%; Pred. No. 0.53;
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POLY-PRO.
POLY-SER.
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POLY-PRO.
POLY-PRO.
MW; 7C5144F443CE6821 CRC64;
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         tumor suppressor candidate region gene 1 protein.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Unknown mitochondrial protein At3g15000.
Arabidopsis thaliana (Mouse-ear cress).
annotation update)
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889
1225
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                               Homo sapiens (Human).
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                                                                NCBI_TaxID=9606;
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1214
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NCBI_TaxI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
Scructural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cbNa clones (RAFLs) sequenced by the
SSP consortium (Salk/Stanford/PGEC).";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
01-DEC-1992 (Rel. 24, Last annotation update)
1-DEC-1992 (Rel. 24, Last annotati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leaf, and Stem;
MEDILIE=216084013, PubMed=11743114;
Kruft V., Eubel H., Jeensch L., Werhahn W., Braun H.-P.,
"Proteomic approach to identify novel mitochondrial proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75;
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SUBCELLULAR LOCATION: Mitochondrial.
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les 46, Conserv
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MEDLINE=92119261; PubMed=1731998;
Dreher T.W., Bransom K.L.;
"Genomic RNA sequence of turnip yellow mosaic virus isolate TYMC, cDNA-based clone with verified infectivity.";
Plant Mol. Biol. 18:403-406(1992).
-i- FUNCTION: NOT KNOWN.
-i- SIMILARITY: TO 65 TO 70 kDa PROTEIN FROM OTHER TYMOVIRUSES.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
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P54259; Q99495; Q99621; Q9UEK7;
1-OCT-1996 (Rel. 34, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Atrophin-1 (Dentatorubral-pallidoluysian atrophy protein).
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Interpro, IPRO04935; Tymo 45 70kDa.
Pfam: PF03251; Tymo 45kd 70kd; 1.
SEQUENCE 628 AA; -69057 MW; ODFOC64E8ECBC6DC CRC64;
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24.0%; Pred. No. 0.24;
tive 21; Mismatches
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TISSUE-Brain, and Cerebellum;
MEDLINE-95144175; PubMed=7842016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=96026098; PubMed=7485154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X16378; CAA34414.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. The European Bioinformatics Institute. The sit on a restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@ibs.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease.
DISBASE: Defects in DRPLA are the cause of dentatorubral-
DISBASE: Defects in DRPLA) [MIM.125370], an autosomal dominant
pallidoluysian arrophy (DRPLA) [MIM.125370], an autosomal dominant
neurodegenerative disorder characterized by a loss of neurons in
the dentate nucleus, rubrum, glogus pallidus and Luys' body.
Clinical features are myoclonus epilepsy, dementia, and cerebellar
ataxia. Onset of the disease occurs usually in the second decade
of life and death in the fourth.
CAUTION: Ref.2 sequence differs from that shown due to several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYMORPHISM: The poly-Gln region of DRPLA is highly polymorphic (7 to 23 repeats) in the normal population and is expanded to about 49-75 repeats in DRPLA patients. Longer expansions result in earlier onset and more severe clinical manifestations of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-76 FROM N.A.

MEDLINE=97005364; PubMed=8852663;
Yanagisawa H., Fujii K., Nagafuchi S., Nakahori Y., Nakagome Y.,
Akane A., Nakamura M., Sano A., Komure O., Kondo I., Jin D.K.,
Soerensen S.A., Potter N.T., Young S.R., Nakamura K., Nukina N.,
Magao Y., Tadokoro K., Okuyama T., Miyashita T., Inoue T.,
Kanazawa I., Yamada M.;
A. unique origin and multistep process for the generation of expanded
Onodera O., Oyake M., Takano H., Ikeuchi T., Igarashi S., Tsuji S., "Molecular cloning of a full-length cDNA for dentatorubral-pallidoluysian atrophy and regional expressions of the expand alleles
                                                                                                                                                                                                                                                                                                                                                                                        Ansari-Lari M.A., Shen Y., Muzny D.M., Lee W., Gibbs R.A.;
"Large-scale sequencing in human chromosome 12p13: experimental and
computational gene structure determination.";
Genome Res. 7:268-280(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain cortex;
MEDLINE=9315145; PubMed=8325628;
MEDLINE=9315145; PubMed=8325628;
Li S.-H., McInnis M.G., Margolis R.L., Antonarakis S.E., Ross C.A.;
"Novel triplet repeat containing genes in human brain: cloning,
expression, and length polymorphisms.";
Genomics 16:572-579(1993).
-!- TISSUE SPECIFICITY: Relatively high levels in the brain, ovary,
testis and prostate. Lower levels in the liver, thymus and
                                                                                                                                                         MEDLINE=96262314; PubMed=8965642;
Margolla R.L., Li S.-H., Young W.S., Wagster M.V., Stine O.C.,
Kidwai A.S., Ashworth R.G., Ross C.A.;
"DRPLA gene (atrophin-1) sequence and mRNA expression in human
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND POLYMORPHISM OF POLY-GLN REGION
                                                                                                                                                                                                                                                                         Brain Res. Mol. Brain Res. 36:219-226(1996)
                                                                                          J. Hum. Genet. 57:1050-1060(1995).
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EMBL; D38529; BAA0734.1; ALT_FRAME.
EMBL; U2381; AAB50276.1; -.
EMBL; U47924; AAB51321.1; -.
EMBL; D63808 BAA23331.1; -.
EMBL; L10377; -; NOT_ANNOTATED_CDS.
PIR; G01763; G01763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A triplet repeats."; Mol. Genet. 5:373-379(1996).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97228904; PubMed=9074930;
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SEQUENCE FROM N.A.
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30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Trophinin-associated protein (Tastin) (Trophinin-assisting protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Trophinin and tastin, a novel cell adhesion molecule complex with potential involvement in embryo implantation."; Genes Dev_9:1199-1210(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                    Length 1185;
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Fukuda M.N., Sato T., Nakayama J., Klier G., Mikami M., Aoki
Nozawa S.;
                              GO:0005/37; C:cytoplasm; TAS.
GO:0005634; C:nucleus; TAS.
GO:0005515; F:protein binding activity; TAS.
GO:0007417; P:central nervous system development; TAS.
                                                                                                                                                                                                       (MIXED CHARGE).
(MIXED CHARGE).
                                                                                                                                                                                                                                            -> Y (IN REF. 1).

-> I (IN REF. 3).

-> T (IN REF. 6).

-> G (IN REF. 1).

-> 5135744CEE491C18 CRC64;
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H -> Y (IN REF. 1).
M -> I (IN REF. 3).
P -> T (IN REF. 5).
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   Genew; HGNC:3033; DRPLA
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 NGIP-----EPQVYAPPRPTDRLAVPPFAQRERFHRFQPTY--PYLQHEIDLPPTI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSARLGGPCPPSSNSGISATCYGSGCRMEGPPPTYSEVIGHYPGSSFQHQ--QSSGPPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | | | | : : | | | | | EQLEVPEPCPAEPGPLQPSTQGQSG-PPGPCPRVE--LGASEPCTLEHRSLESSLPPCC 662
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FUNCTION: COULD BE INVOLVED WITH BYSTIN AND TROPHININ IN A CEL
ADHESION MOLECULE COMPLEX THAT MEDIATES AN INITIAL ATTACHMENT
THE BLASTOCYST TO UTERINE EPITHELIAL CELLS AT THE TIME OF THE
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4 X 33 AA APPROXIMATE TANDEM REPEATS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                    SUBUNIT: DIRECTLY BINDS BYSTIN, AND INDIRECTLY TROPHININ. SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: STRONG EXPRESSION AT IMPLANTATION SITES.
EXCLUSIVELY LOCALIZED TO THE ARICAL SIDE OF THE SYLOCYTIOTROPHOBLAST. ALSO FOUND IN MACROPHAGES.
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15-SEP-2003 (Rel. 42, Last annotation update)
Endothelial cells scavenger receptor precursor
SCANFORD SREC OR KIAA0149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
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Pred. No. 0.46;
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TISSUB-Umblical vein endothelial cells;
MEDLINE-98058897; Pubmed=3995444;
Adachi H., Tsujimoto M., Azai H., Inoue K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
Cell adhesion; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SREC HUMAN STANDARD;
014162; 043701;
28-FEB-2003 (Rel. 41, Created)
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Genew; HGNC:12327; TROAP.
                                                                                              IMPLANTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 6
778 AA;
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b-17.rsp

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60; Conservative
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                                                                                                                                                            830 AA;
                                                                                                                                                                                    Similarity
 V70K TYMV
P10357;
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                                                                                                              DISULFID
                                                                                                                                                     CONFLICT
         SULFID
                                SULFID
                                                       SULFID
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V70K_TYMV
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                      EMBL; D86864; BAA24070.1; -.

R EMBL; D86864; BAA29770.1; -.

R HSSP; P01180; 2BN2

R HSSP; P01180; 2BN2

R Gonew; HGNC:16820; SCARF1.

GO; GO:0004888; F: Cansemenbrane receptor activity; IDA.

GO; GO:0004888; F: Low-density lipoprotein binding activity; IDA.

GO; GO:0006888; F: Low-density lipoprotein catabolism; TAS.

R GO; GO:0006889; P: receptor mediated endocytosis; TAS.

R InterPro; IPR006209; EEF like.

R InterPro; IPR006210; IEGF

R InterPro; IPR006210; IEGF

R InterPro; PR0001; EGF-AMININ.

R SWART; SW0011; EGF-AMININ.
                                             Adachi H., Tsujimoto M.; "Characterization of the human gene encoding the scavenger receptor expressed by endothelial cell and its regulation by a novel transcription factor, endochelial zinc finger protein-2."; J. Biol. Chem. 277:24014-24021(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENDOTHELIAL CELLS SCAVENGER RECEPTOR EXTRACELLULAR (POTENTIAL).
"Expression cloning of a novel scavenger receptor from human endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01186; EGF 2; 6.
Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
EGF-like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
PRO/SER-RICH.
GLY-RICH.
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POTENTIAL.
POTENTIAL.
                Biol. Chem. 272:31217-31220(1997).
                              SEQUENCE FROM N.A.
MEDLINE-22086180; Pubmed=11978792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830
4421
8442
830
87
130
                                                                                           SEQUENCE FROM N.A.
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53
95
215
215
3302
3476
622
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 QVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPY----QG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 PCTLÓLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMEGPPPTYSEVIGHYPGSSFQHQQSSGP-----PSLLEG-TRLHHTHIAPLESA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RR--PPLGSRTVAEHVEAIEGSVQESSGPVTTIYMLAGKPRGSEGPVRSVFRHFGSFQKG 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508 SFIEPPSAGWATDDSFSSDPESGEADEVPAYCVPPOEGMVPVAQAGSSEASLAAGAFPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 EDASTP----FAIPRTSSLARAKR-----PSVSFAEGTKFAPQSRRSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : || |:: |:| || ELSSPLKKPKR----LSRGAQSGPEGREAEESTGPDEAEAPESFPAAASPGDSAT----GH
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MEDLINE=88289359; PubMed=3399388;

Morch M.D., Boyer J.C., Haenni A.L.;

"Overlapping open reading frames revealed by complete nucleotide sequencing of turnip yellow mosaic virus genomic RNA.";

Nucleic Acids Res 16:6157-6173(1988).

-!- FUNCTION: NOT KNOW.

-!- FUNCTION: TO 65 TO 70 kDa PROTEIN FROM OTHER TYMOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 km protein.
Turnip yellow mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
VCBI _TaxID=12154;
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                                                                                                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 104; DB 1; Length 830; 22.6%; Pred. No. 1.5; Live 32; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                         POTENTIAL.

N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
R -> W (IN RRF. 3).

4, F560D9EIAA64D779 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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Pfam; PF00568; WH1;
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                                                                                                                                                                      11;
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       536
                                                                                                                                                                                                                     40 RHSQGRRREDALSSEGCLWPSESTVSGNG----IPE---POVYAPPRPTDRLAVPPFAO
                                                                                                                                                                                                                                                             92 RERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELN-----
                                                                                                                                                                                                                                                                                           -------PQLPLRDLGRTPGFPTPPKTPTRTPESRITASPTDIAPL
                                                                                                                                                                                                                                                                                                                         145 -----RESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPT
                                                                                                                                                                                                                                                                                                                                                       -- POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: FOCAL ADHESIONS.
PIM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT PROTEIN KINASE (CGPK) IN PLATELETS.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning, structural analysis and functional expression of
the proline-rich focal adhesion and microfilament-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ACTIN- AND PROFILIN-BINDING MICROFILAMENT-ASSOCIATED PROTEIN. MAY ACT IN CONCERT WITH PROFILIN TO CONVEY SIGNAL TRANSDUCTION TO ACTIN FILAMENT PRODUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                     488 DSDPVLSVRTEVHAPERRIFMDPEALRSALASLPSPPRS-VGIIHTA-----
                                                                                                                                                                                                                                                                                                                                                                                   197 YSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKD 245
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95129547; PubMed=7828592;
Haffner C., Jarchau T., Reinhard M., Hoppe J., Lohmann S.M.,
                                                                                                                                        Length 628;
                                                                                                                                                                      Indels
                                                       PIR; S01955; S01955.
InterPro; IPR004935; Tymo 45 70kDa.
Pfam; PF03251; Tymo 45kd 70kd; 1.
SEQUENCE 628 AA; 69195 MW; 9B01CESADFCEAC77 CRC64;
                                                                                                                                                                  80;
                                                                                                                                      7.6%; Score 103; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Vasodilator-stimulated phosphoprotein (VASP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 AA
                                                                                                                                                                    19; Mismatches
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                                                                                                                                                       Pred. No.
                                             EMBL; X07441; CAA30321.1; ALT_SEQ.
                                                                                                                                                    25.3%;
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PIR, S51796; S51796.
InterPro; IPR000697; EVH1.
                                                                                                                                                                      Conservative
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                                                                                                                                                    Local Similarity
tes 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
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                                                                                                                                        Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ------GPPPPPGVSLSGGSAAGHGAGG---GPPPAPPLPTAQGTSGGGTGAPGLAA 231
                                                                                                                                                                                                                                                                                                      47 REDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQR-ERFHRFQPTYP-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARKEDLY REDUCED AMOUNTS ARE FOUND IN MOST OTHER TISSUES.
DEVELOPMENTAL STAGE: SIMILAR EXPRESSION AT ALL DEVELOPMENT STAGES
(DAY 14.5 P.C., 17.5 P.C., NEWBORNS AND ADULTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                159 SDLMDSARLGGPCPPS-SNSGISATCYGSGGRMEGPP----PTYSEVIGHYPGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                     74; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loev S.J., Margolis R.L., Young W.S., Li S.-H., Schilling G., Ashworth R.G., Ross C.A.; "Cloning and expression of the rat atrophin-I (DRPLA disease gene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE Erain, Cerebellum, Hippocampus, and Substantia nigra; PubMed-851849; Schultt I. Epplen J.T., Riess O.; Schmitt I. Epplen J.T., Riess O.; "Predominant neuronal expression of the gene responsible for "Predominant neuronal expression of the gene responsible for dentacroubral-pallidolugatan atrophy (DRPLA) in rat."; Hum. Mol. Genet. 4:1619-1624 (1995).
                                                                                      (BY
                                                                                                                         (BY
                                                                                                                                                          (BY
                               POLY-PRO.
POLY-BRO.
POLY-SER.
POLY-SER.
SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKG)
                                                                                                                                                            PHOSPHORYLATION (BY PKA AND PKG)
                                                                                                                                                                                                                                Score 101; DB 1; Length 384; Pred. No. 1.1;
                                                                                                                                                                                                                                                                   64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atrophin-1 (Dentatorubral-pallidoluysian atrophy protein)
                                                                                                                                                                                             266BB3C46FB4397F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         155 LERRVSNAGGPPAPP----AGGPPPPPGPPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 AIAGAKLRKVSKÓEEAŚGĠPPVPKAESTR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SPQHQQSSGPP-SLLEGTR 225
                                                                                                                                                                              SIMILARITY)
                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Cerebellum, and Striatum;
MEDLINE=97317138; PubMed=9173996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurobiol. Dis. 2:129-138(1995).
                  Phosphorylation; Actin-binding.
DOMAIN 118 124 PC
DOMAIN 173 189 PC
                                                                                                                                                                                               384 AA; 40413 MW;
                                                                                                                                                                                                                                7.5%;
                                                                                                                                                                                                                                                                   55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                      124
189
329
                                                                                                                                                              281
                                                                                                                           242
SMART; SM00461; WH1;
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                    326
                                                                                                                         242
                                                                                                                                                            281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRPL RAT
                                                                                        MOD_RES
                                                                                                                                                            MOD RES
                                                                                                                         MOD_RES
                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SLPSQAVWSQ 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 DLMDSARLGGPCPPSSNSGISATCYGSGGRMEGP-PPTYSEVIGHYPGSSFQHQQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GPPPPPPYG---RLLPNNNTHPGPFPPTGGQSTAHPPAPAPAHHHQQQQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 kDa protein.
Turnip yellow mesaic virus (Australian isolate).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
NCBI_TaxID=12155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90021184; PubMed=2800335;
Keese P., Mackenzie A., Gibbs A.;
"Nucleotide sequence of the genome of an Australian isolate of
                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: TO 65 TO 70 kDa PROTEIN FROM OTHER TYMOVIRUSES
                                                                                                                                                                                                                                                                                          N -> S (IN REF. 2).
F -> L (IN REF. 2).
P -> R (IN REF. 2).
T -> M (IN REF. 2).
A -> V (IN REF. 2).
MISSING (IN REF. 2).
MM; 7FB9928DCADF9B1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 PSYPH----SFPPPTSMSVSNQPPKYTOP------
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 ------SSGP-----PSLLEGTRLHHTH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 QPQPQPQHHHGNSGPPPPGAYPHPLESSNSHHAH 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 100.5;
22.6%; Pred. No. 4.1
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                                                                                                                                                            POLY-PRO.
POLY-SER.
POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                   124778 MW;
                                                                                      EMBL; X89453; CAA61623.1; -.
InterPro; IPR002951; Atrophin.
Pfam; PF03154; Atrophin-1; 2.
                                                                       EMBL; U3177; AAA80337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 172:536-546(1989)
                                                                                                                                  PRINTS; PR01222; ATROPHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tymovirus.
                                                                                                                                                                                                                                                                              705
455
594
689
717
                                                                                                                                                              306
383
391
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                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yellow mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V70K TYMVA
P20131;
                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RH---RRSHPLLPNPPAALPPIAYTSGRGKIHHSLPKGALPKEGPPPPRRLPSPATPPQ 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 AQRERFHRFQPTYPYLQHEIDLPPTISLSDGEE----PPPYQGPCTLQLRDPEQQLELNR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 ESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546
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MEDLINE=99375328; PubMed=10444336;
Nagaya T., Chen K.-S., Fujieda M., Ohmori S., Richer J.K.,
Horwitz K.B., Lupski J.R., Seo H.;
"Localization of the human nuclear receptor co-repressor (hN-COR) gene
between the CMTIA and the SMS critical regions of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         some
                                                                                                                                                                                                                                                                                                                                                                     40 RHSQGRRREDALSSEGCLWPSESTVSGNG-----IPEPQVYAPPRPTDRLAVPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLRDLGR-TPSFP-----DSDPVLSV-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 59:339-341(1999).

-!- FUNCTION: Mediates the transcriptional repression activity of inclear receptors by promoting chromatin condensation, thus preventing access of the basal transcription.

-!- SUBUNIT: Interacts with HDAC7 (By similarity). Forms a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
MEDLINE=98393736; PubMed=9724795;
WEDLINE=98393736; PubMed=9724795;
Wang J., Hoshino T., Redner R.L., Kajigaya S., Liu J.M.;
Wang J., Hoshino T., Redner R.L., Kajigaya S., Liu J.M.;
"ETO, fusion partner in t (8;21) acute myeloid leukemia, represses transcription by interaction with the human N-CoR/mSin3/HDAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497 TEVHAPERRIFMDPEALRAALAGLPSPPLS-VGIIRTASQTVLPTNSPSPT-
                                                                                                                                                                                                                              7.4%; Score 100; DB 1; Length 628; 55.0%; Pred. No. 2.2; ve 19; Mismatches 92; Indels
                                                                                          InterPro; IPR004935; Tymo 45 70kDa.
Pfam; PF03251; Tymo 45kd 70kd; 1.
SEQUENCE 628 AA; 68740 MW; 67CD342A09161D96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 95:10860-10865(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCR1 HUMAN STANDARD; PRT; 2440 AA. 075376; Q9UPV5; Q9UQ18; Created) 16-OCT-2001 (Rel. 40, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Nuclear receptor co-repressor 1 (N-COR1) (N-COR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99397452; PubMed=10470851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for large proteins in vitro.";
DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 782-2440 FROM N.A.
                               EMBL; J04373; AAA46591.1; -. PIR; JQ0110; JQ0110.
                                                                                                                                                                                                                                                                    25.0%;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                           Local
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NCR1 HUMAN
                                                                                                                                                                                                                                                                    Best Loc
Matches
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                              (2)
CHARACTERIZATION.
                                                                                                                                                                                                                21-JUL-1986
                                                                                                                                                                                                                                                             BERF3-BERF4.
                                                           195
                                                                                                                                                                                         EBN6 EBV
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                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PSESTVSGNGIP----EPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERD 845
          HDACI and HDAC2. This complex associates with the thyroid (TR) and the retinoid acid receptors (RAR) in the absence of ligand. SUBCELLULAR LOCATION: Nuclear (By similarity).

DOWAIN: The N-terminal region contains repression functions that are divided into three independant repression domains (RD1, RD2 and RD3). The C-terminal region contains the nuclear receptorinteracting domains that are divided in two separate interaction domains (ID1 and ID2).

DOMAIN: The two interaction domains (ID) contain a conserved
corepressor complex that contains SIN3A/B and histone deacetylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     738 PENATSRGNTEPAVELEPTTETAPSTSPSLAVP-----STKPAEDESVETQVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 ISLS-----DGEE-----PPP--YQGPCTLQLRDPE-----QQLE
                                                                                                                   sequence referred to as the cornr box. This motif is required and sufficient to permit binding to unliganded TR and RARS. Sequences flanking the CORNR BOX determine nuclear hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                               SIMILARITY: Contains 1 SANT-A domain.
SIMILARITY: Contains 1 Myb-like domain.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Transcription regulation; DNA-binding; Repressor; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100; DB 1; Length 2440;
                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T04687; ...
Genew, HGMC: 7672; NCOR1.
MIM; 600849; ...
GO; GO:0003714; F:transcription co-repressor activity; TAS.
GO; GO:000366; P:transcription from Pol II promoter; TAS.
InterPro; IPRO10105; Myb DNA binding.
PF00249; myb_DNA-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60A4D7964D00EDAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH SIN3A/B.
COILED COIL (POTENTIAL).
SANT-A (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L -> V (IN REF. 2).
PP -> SS (IN REF. 2).
W -> R (IN REF. 2).
Q -> H (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH ETO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOX OF ID1.
BOX OF ID2.
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37; Mismatches
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POLY-PRO.
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POLY-SER.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINES 48270667; PubMed=6087149;
MEDLINES 48270667; PubMed=6087149;
Back R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome:";
Nature 310:207-211 (1984).
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                                     143 LNRESVRAPPNRTIFDSDLMDSARLGGPCP-PSSNSGISATCYGSGGRMEGPP----
                                                                                                                                          ---LEGTRLH
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Petti L., Sample J., Wang F., Kieff E.;
As fifth Esptein-Barr virus nuclear protein (EBNA3C) is expressed : latently infected growth-transformed lymphocytes.";
J. Virol. 62:1330-1338(1988).
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
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                                                                                                                                          --FOHOOSSGPPSL----
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3 X 13 AA TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
EBNA-6 nuclear protein (EBNA-3C) (EBNA-4B).
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|QRHIKAMHESALLEEQRQRQE 981
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(Rel. 08, Last sequ
(Rel. 28, Last anno
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71 EPQVYAPPRETURLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPC 130 131 TLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGS---- 186 187 -----GGRMEGP-----PPTYSEVIGHYPG--SSPQHQQS-SGPPSILEGTRLHHT 229 230 HIAPL--ESAAIWSKEKDKOKGHPL 252 : || || || : : |: 865 SLVPLVSSSAPSWSSPQPRAPIRPI 889 8 8 8 a 8 6 g ઠે

Search completed: December 4, 2003, 19:50:45 Job time : 20 secs

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b-17.rspt

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

December 4, 2003, 19:48:04; Search time 35 Seconds (without alignments) 1857.979 Million cell updates/sec Run on:

US-09-857-826B-17 1348 1 MAELEFVQIIIIVVVMMVMV......PLESAAIWSKEKDKQKGHPL 252

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

830525 segs, 258052604 residues Searched:

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:\* Database :

sp archea:\*
sp bacteria:\*
sp bucteria:\*
sp fungl:\*
sp human:\*
sp invertebrate:\*
sp mammal:\*
sp organele:\*
sp organele:\* 12::13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

SUMMARIES

SOUTHERIES			Description	Q8ner4 homo sapien	OBbye2 mus	OBbwi4 mus	O8r5e2 mus	O9by18 homo	Ogntr9 homo	, Q8izll homo	Q96ai8 homo	O8iz34 homo	Q8n6w3 homo	075114 homo			18 Q8cfs8 mus musculu	77 O817d7 arabidopsis	091vk5
200			ΩI	Q8NER4	Q8BYE2	OBBWJ	QBRSE2	Q9BYL8	Q9NTR9	OBIZE	096AI8	Q81Z34	Q8N6W3	075114	OBVZRB	9M0H8	QBCFSB	Q8L7D7	Q9LYK5
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			Match Length DB	237	292	306	200	53	84	593	494	607	634	634	496	508	462	357	530
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			Score	1282	820.5	817.5	662.5	252	244	126	125.5	125.5	125.5	125.5	123.5	123.5	123	122	122
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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM:
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Mature 420:563-573(2002).
EMBL; AK040289; BAC30562.1; -.
SEQUENCE 292 AA; 32521 MW; F780D391984D66E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Heart;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Henome Exploration Research Group Phase I & II Team;
Manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 42<u>0.5</u>63-573(2002).
181 TYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMD-SARLGGPCPPSSNSGIS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein C180RF1 homolog.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%; Score 820.5; DB 11; Length
63.6%; Pred. No. 7.1e-72; '
Live 24; Mismatches 45; Indels
                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                           Created)
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                                                                                                               PRT;
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279 VPI-----KGKDRKPG 289
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                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.69
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                          Protein C18ORF1 homolog.
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Q8BWJ4
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                                                                                                                                    ACCOCO DE LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA PACA LA P
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                                                                                                                                                                                                             61 SELEFAQILIIVVVVVTVMVVVVVCLLNHYKVSTRSFINRPNQSQRQEDGLQPEGSLWPSD 120
                                                                                                                                                                                                                                                                                                         239 AATCSSNGRMEGPPPTYSEVMGHYPGTSFFHHQHSNTHRGSRPQFQPNNSEGT----1 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMD-SAR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 EIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQMELNRESVRAPPNRTVFDSDLIDISMY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                    STVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGE
                                                                                                                                                                                                                                                                                                                                                                                      EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMD-SARLGGPCPPSSNSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 LGGPCPPSSNSGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQQSSG-----P
                                                                                                                                                                             2 AELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSG------PPSLLEGTRLHHTHI
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amnotation update)
Similar to chromsome 18 open reading frame 1 (Fragment).
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Muscul-TaxID=10090;
                                                                                                                           25;
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                                                                       60.6%; Score 817.5; DB 11; Length 63.2%; Pred. No. 1.5e-71; ive 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.1%; Score 662.5; DB 11; Length 62.7%; Pred. No. 1.2e-56; artive 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; EC022716; AAH22716.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AA; 22117 MW; 14A78F6E8A4C09A5 CRC64;
EMBL; AKOS2338; BAC34943.1; -.
SEQUENCE 306 AA; 33857 MW; 043C2260AEE8729F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLLEGTRLHHTHIAPLESAAIWSKEKDKQKG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 VPI-----KGKDRKPG 303
                                                                                                                           Matches 163; Conservative
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
DJ1059L7.1.2 (Androgen induced type 1b transmembrane protein (PMEPA1), isoform 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ1059L7.1.1 (Androgen induced type 1b transmembrane protein (PMEPAl),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                            Skuce C.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AL121913; CAB88144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
6064 MW; A3B563FB81F69782 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 AA; 9236 MW; 7FCFCF1FFBEFBC92 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 18.7%; Score 252; DB 4; Stailarity 100.0%; Pred. No. 2.6e-17; 53; Conservative 0; Mismatches 0;
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01-MAR-2003 (TrEMBLrel. 23, Last seque
01-MAR-2003 (TrEMBLrel. 23, Last annot
Mucoepidermoid susceptibility protein.
MECTI.
Homo sapiens (Human).
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                                                                                                                                                                            Homo sapiens (Human)
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Matches 53; Conserv
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                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
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Q9NTR9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 FSP---GSSPQLEQFNWMENAISSSSLYS-----PGSTLNYSQAAMMGLTGSHGSLPDS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 QLRDPEQ------QLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 PQSPPENPGQPSMGIDIASAPALQQYRTSAGSPANQS------PTSPVSNQG 327
                                                                                                                                                                                                                                                                                                                                                                         ----DALSSEGCLWPSESTVSGNGIPEPQVYAPPRP
                                                                                                                                                                                                                                                                                                       314 LSLSTEARRQQASPTLSPLSPITQAVAMDALSLEQQLPYAFFTQAGSQQPPPQPPPPP
                                                                                                                                                                                                                                                                                                                                              81 TORLAVPPFAORERFHRFOPTYPYLQHEIDLP-----PTISLSDGEEPPP--YQGPCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 POSPPENPGOPSMGIDIASAPALOQYRTSAGSPANOS-------PTSPVSNOG
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                                                                aberrant
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            98;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Tonon G., Modi S., Kubo A., Coxon A., Kirsch I., Kaye F.J.;
Tonon G., Modi S., Kubo A., Coxon A., Kirsch I., Kaye F.J.;
Tonon G., Wapping between MAML2 and MECTI suggests a role for NOTCH signaling in the genesis of mucoepidermoid tumors.",
Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY040323, AAK93832.1, -
SEQUENCE 593 AA, 62529 MW; B7DB709B0C731D29 CRC64,
                                                                                                                                                                                Query Match
9.3%; Score 126; DB 4; Length 593;
Best Local Similarity 24.6%; Pred. No. 0.001;
Matches 68; Conservative 30; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BEC017075; AAH17075.1; -.
InterPro; IFR012965; P rich extensn.
PRINTS; PR01217; PRICHEXTENSN.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
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Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                 38 ISRHSQGRRRE-----
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TISSUE=Colon;
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Q96AI8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 LSLSTEARRQQASPTLSPLSPITQAVAMDALSLEQQLPYAFFTQAGSQQPPQPPPPPP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 -----PPASQQ------PPPPPPPQAPVRLPPGGPLLPSASLIRGPQPPPLAVIVPSSL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 QLRDPEQ-----QLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 ISRHSQGRRRE-------DALSSEGCLWPSESTVSGNGIPEPQVYAPPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75; Gaps
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 125.5; DB 4; Length 607; 24.7%; Pred. No. 0.0012; ive 24; Mismatches 63; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023614; AAH23614.1; -.
Hypothetical protein.
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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INCEPPO; IPRO2956; P. rich extensn.
PRINTS; PR01217; PRICHETRENSN.
SEQUENCE 634 AA, 67269 WW; BCDS3DD389D041DE CRC64;
                                                                                                                                                                                                                              (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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I-OCT-2002 (TrEMBLrel. 22, Last sequence update)
I-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                   179 ISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 ISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PGSSPQHTSTLGSVFGDAYYEQQ 465
                                                               328 FS------PGSSPQHTSTLGSVFGDAYYEQQ 352
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01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical protein (Fragment).
Homo sapiens (Human).
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Best Local Similarity 24.7
Matches 53, Conservative
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                                                                                                                                                                                                                                             ---QLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSG 178
                                                                                                                                                                                                                                                                                              -----PTSPVSNQG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 IDRLAVPFFAQRERFHRFQPTYPYLQHEIDLP-----PTISLSDGEEPPP--YQGPCTL 132
                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...--DALSSEGCLWPSESTVSGNGIPEPOVYAPPRP 80
                                                                               81 TDRLAVPPFAQRERFHRFQPTYPYLQHEIDLP----PTISLSDGEEPPP--YQGPCTL
                                                                                                                                                                                   ----DALSSEGCLWPSESTVSGNGIPEPQVYAPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLSTEARRQQASPTLSPLSP1TQAVAMDALSLEQQLPYAFFTQAGSQQPPPQPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE-994038

Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,

Nomura N., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. X.

The complete sequences of 100 new cDNA clones from brain which can

code for large proteins in vitro.";
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 27-440 FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamkhart-Schultz K., Gordon L., Dias J., Kyle A., Brower A.,

Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,

Garnes J., Danganan L., Erler A., Christensen M., Georgescu A.,

Avila J., Liu S., Attix C., Andreise T., Trankheim M.,

Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,

Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D.

Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;

"Sequence analysis of a 1.9 Mb contig in 19pl2 between UBA52 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75;
75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 634 AA; 66992 MW; C2D3BE373C0979A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein KIAA0616 (Fragment).
                                                                                                                                                                                                                                                                                                422 POSPPENPGQPSMGIDIASAPALQQYRTSAGSPANOS----
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                          ------PGSSPQHTSTLGSVFGDAYYEQQ 492
                                                                                                                                                                                                                                                                                                                                                 179 ISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.3%; Score 125.5; DB 424.7%; Pred. No. 0.0013; ative 24; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB014516; BAA31591.1; -. EMBL; AC006123; AAC97072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 08, (TrEMBLrel. 08, (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                38 ISRHSQGRRRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 ISRHSQGRRRE-
                                                                                                                                                                                                                                                133 QLRDPEQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
  53;
                                                                                                                                                                                                                                                                                                                                                                                                  468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                               374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D19S455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA0616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       075114
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4

Length 634;

9.3%; Score 125.5; DB 4; 24.7%; Pred. No. 0.0013;

Query Match Best Local Similarity b-17.rspt

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467
133 QLRDPEQ------QLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 PĠNQPPVESLPSSMQMQSPYSĠP-----PQÓSMQAYGYGAAPPPQAPPQQTKMSYSPQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LG-----GPCPPSSNSGISATCYGSGGRMEGPP--PTYSEVIGHY-----PGSSFQHQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 TGDGYLPSGPPP---SGYANAMY-EGGRMQYPPPQPQQQQQQAHYLQGPQGGGYSPQPH 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
Yamamura Y., Yu G., Yu S., Bower L., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                       --- PTSPVSNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPQVYAPPRPTDRLAVPP-----FAQRERFHRFQPTYP----YLQHEIDLPPTISLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 PPSQLQAPPAQSQFMPPPPAPSHPSSAQTQSFPQYQQNWPPQPQARPQSSGGYPTYSPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGEEPP-----PYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSAR
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carnino P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Bakurai T., Satou M., Shim N., Shim P., Southwick A., Shinozaki J. Shabasis R.W., Ecker J.R., Theologis A., Suthwick A., Shinozaki J. Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%; Score 123.5; DB 10; Length 26.4%; Pred. No. 0.0015; tive 18; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Full Length cDNA of gene At4g28300 (GI:15235249).", Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1BF54098B9A79429 CRC64;
                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                 179 ISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQ 213
                                   422 POSPPENPGOPSMGIDIASAPALQOYRTSAGSPANOS-
                                                                                                                                                                                                                                                                                                                         AT4G28300.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ); IPR002965; P rich extensn.
PR01217; PRICHEXTENSN.
: 496 AA; 54106 MW; 1BF540
                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                         Putative proline-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY096387; AAM20028.1; -.
                                                                                                                                                                                                                                               (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSSG-----PPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 QAGGGNIGAPPVL 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Conservative
                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinn P., Sout
Theologis A.;
                                                                                                                                                                                                                                               01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
PRINTS; PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                          OBVZRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 DGEEPP------PYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSAR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 PGNQPPVESLPSSMQMQSPYSGP-----PQQSMQAYGYGAAPPPQAPPQQTKMSYSPQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 TGDGYLPSGPPPP---SGYANAMY-EGGRMQYPPPQPQQQQQAHYLQGPQGGGXSPQPH 439
                                                                                                                                 Argarioppis chaildha (Mouse-ear Cress).
Ekaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopphyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 LG------GPCPPSSNSGISATCYGSGGRMEGPP--PTYSEVIGHY-----PGSSFQHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPQVYAPPRPTDRLAVPP-----FAQRERFHRFQPTYP-----YLQHEIDLPPTISLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                    В.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Lennard N., Quail M., Harris B., Rajandream M.A., Barrell
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                     EU Arabidopais sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AL161572; CABF9632.1; -.
Interpro; IFR002965; P rich extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 508 AA; 55574 MW; 0C5C6C09926Al164 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jasouron, Strandberg R.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC038012; AAH38012.1; -. Hypothetical protein. SEQUENCE 462 AA; 51056 WW; 42D511ECC74E228E CRC64;
                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Predicted proline-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein FLJ12529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; Score 123.5; DB 10; 26.4%; Pred. No. 0.0015; tive 18; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 123; DB 11;
Pred. No. 0.0015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 AA
                                                                                                                          Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 QSSG----PPSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 QAGGGNIGAPPVL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 26.4
les 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Eye;
                                                                                                     AT4G28300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBCFSB
Q9M0H8
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Q8CFS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SOUTHWICK A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,

A Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

Deng J.M., Hayashizaki Y., Hauan V.W., Lee J.M., Ishida J., Kamiya A.,

Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,

Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,

M. Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,

Theologis A., Davis R.W.;

L. Submitted (JUL.-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AX136314; AAM96980.1; -.

R. InterPro; IPR002465; P. rich extensn.

R. InterPro; IPR002465; P. rich extensn.

R. RILLSTP PRICHEKTENSN.

R. Hypochetical protein.

W. Hypochetical protein.
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                                                               68 ----GIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEP 123
                                                                                                                                                                                            124 PPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATC 183
                                                                                                                                                                                                                                   272 PPGAIPPALHL------NPAFFPPPNATV--------GP-PPDTYMKASTPY 308
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                                      67
                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
9.1%; Score 122; DB 10; Length 357;
Best Local Similarity 29.1%; Pred. No. 0.0014;
Matches 48; Conservative 8; Mismatches 71; Indels' 38; Gaps
  Gaps
  60;
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70; Indels
                                      27 LSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGN---
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Last annotation update)
17; Mismatches
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50; Conservative
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Matches
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
| SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:\*
| SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:\*
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| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:\*
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| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1992.DAT:\*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:\*
| SIDSI/gcgdata/gen 1 MAELEFVQIIIIVVVVMMVMV......PLESAAIWSKEKDKQKGHPL (252 Description 1107863 Ø 5.1.6 Compugen Ltd. Total number of hits satisfying chosen parameters: 1107863 segs, 158726573 residues version : SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries - protein search, using sw model AAB18449 AAB01388 ABG61805 ABP75660 AAB18461 AAB18462 AAB18463 AAB18463 AAB18463 BLOSUM62 Gapop 10.0 , Gapext 0.5 GenCore Copyright (c) 1993 seq length: 0 seq length: 200000000 US-09-857-826B-17 23 23 23 23 23 23 23 252 252 252 252 252 252 252 287 287 Length December Query Match 100.0 1000.0 1000.0 99.8 999.8 999.8 Perfect score: Scoring table: 1348 1348 1348 1348 1345 1345 1345 1345 Score OM protein Minimum DB Maximum DB Sequence: Database Run on: Result Š.

(first entry)

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Neuron associated protein; NEUAP; neurological disorder; epilepsy;
                                                         Neuron-associated protein.
                            20-OCT-2000
   AAB01388;
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   The present sequence represents a numan tance tell present sequence represents a numan tance tell present sequence. The representation and/or modulate cellular differentiation and/or modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular interactions, and cell trafficking and/or migration, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and rentrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders because such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cardiovascular disorders such as ischemic heart diseases would be used to treat disorders associated diseases or cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's blassas, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, is and carcers, hydrocephalus and encephalitis, and treat hepatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                        Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                            present sequence represents a human TANGO 261 polypeptide. cification also describes TANGO 266, TANGO 216, TANGO 262, a
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0
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                                                                                                     Fraser CC;
                                                                                                  Sharp JD,
                                  99US-0122458. R
                                                                                                                                                                                                                                 Claim 2; Fig 5; 175pp; English.
                                                                     (MILL-) MILLENNIUM PHARM INC
               01-MAR-2000; 2000WO-US05226.
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Matches 252; Conservative
                                                                                                  Barnes TM, Holtzman DA,
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                                                                                                                               2000-579269/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AA;
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                                          01-MAR-1999;
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                                                                                                                               WPI;
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New human neuron-associated proteins and polynucleotides encoding them, useful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders
ischemic cerebrovascular disease; stroke; cerebral neoplaem; Alzheimer's disease; Pick's disease; Huntington's disease; demvelinating disease; ementala; parknison's disease; Huntington's disease; ementala; prion disease; mentalainating disease; mentalaining prion disease; mentalaining disease; mentalaining prion disease; mentalaining prion disease; muscular dystrophy; central nervous system; CNS; peripheral nervous system; PNS; myopathy; schizophrenia; concinic keratosis; arteriosclerosis; atherosclerosis; atherosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD; myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer; autoimmune disease; inflammation; acquired immunodeficiency syndrome; AlDS; Addison's disease; adult respiratory distress syndrome; allery; ankylosing spondylitis; amyloidosis; anaemia; asthma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Transmembrane region
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/label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Werner syndrome, trauma; human
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99US-0119365.
99US-0124687.
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N-PSDB; AAA47429.
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09-FEB-1999;
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Lu DAM,
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AAB01388 standard; Protein; 252 AA

AAB01388 ID AAB0 XX RESULT 2

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Tue Dec

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spondylitis, amyloidosis, anemia, asthma, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal parasitic, protozoal, and helminthic infections, and trauma. This protein was given the Incyte ID no.
                                                Claim 1, Page 113-114; 145pp; English.
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Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue.

Claim 27; Page 305; 436pp; English.

Mack DH, Wilson KE, Afar D, Hevezi

Gish KC,

2002-471335/50.

N-PSDB; ABK92120

(EOSB-) EOS BIOTECHNOLOGY INC

30-APR-2001; 2001US-0847046. 04-MAY-2001; 2001US-288589P.

2000US-0733288. 2000US-0733742. 2001US-263957P.

24-JAN-2001; 16-MAR-2001;

12-OCT-2001; 2001WO-US32045

WO200230268-A2.

Mammalia

18-APR-2002

2001US-276791P. 2001US-276888P. 2001US-281922P. 2001US-286214P.

16-MAR-2001; 06-APR-2001; 24-APR-2001;

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Query Match
Best Local Similarity 100.
Matches 252; Conservative
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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polymucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are incit.
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ABG61800-ABG61944 represent prostate cancer-associated proteins
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240 240

Prostate cancer-associated protein #6.

15-AUG-2002

XXXEXBXXX

ABG61805 standard; Protein; 252 AA

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SKEKDKQKGHPL 252

ABP75660 standard; Protein; 285 

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ABP75660;

(first entry) 10-FEB-2003

Human secretory polypeptide SPTM SEQ ID NO 844.

Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia; asthma; Crohn; a disease; neurological disorder; epilepsy; cancer; Huntington's disease; neurological disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-tiplammatory; immunosuppressive; neuroporotective; notropopic; neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein.

Homo sapiens

WO200283876-A2

24-OCT-2002

27-MAR-2002; 2002WO-US09921

29-MAR-2001; 2001US-280068P. 16-MAY-2001; 2001US-291280P. 29-MAR-2001; 2001US-280067P

17-MAY-2001; 2001US-291829P. 17-MAY-2001; 2001US-291849P. 19-UUN-2001; 2001US-29428P. 20-UUN-2001; 2001US-39076B. 20-JUN-2001; 2001US-300001P.

(INCY-) INCYTE GENOMICS INC

Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Rleefeld Y, Gerstin EH;
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME; Dafto A,
Dufour GE, Hillman, C.,
Daughtery SC, Dam TC,
TC, David MH, Flores V, Marwaha R,

WPI; 2003-075543/07.

N-PSDB; ABZ36103

diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or cancers New human secretory proteins and polynucleotides, useful for

Claim 27; SEQ ID NO 844; 458pp + Sequence Listing; English.

The invention relates to a secretory polynucleotide (designated sptm)

comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a

meturally occurring polynucleotide sequence at least 90 % identical to

the polynucleotide sequence, a polynucleotide complementary to them or an

ENA equivalent of them. The polypeptide or polynucleotide are useful for

treating, preventing or diagnosing a disease or condition associated with

the expression of functional SPTM. These are particularly useful for

diagnosing, treating or preventing autoimmune/inflammatory disorders

(e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's

disease), neurological disorders (e.g. epilepsy, Huntington's disease,

dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,

multiple sclerosis, crebral palsy, Parkinson's disease,

multiple sclerosis, crebral palsy, Parkinson's disease,

schizophrenia or amnesia), or cell proliferative disorders (e.g.

psoriasis, polycythemia vera, or call proliding adenocarcinoma,

leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,

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breast, cervix or prostate). The present sequence is one of the SPTM proteins of the invention (ABP75384-ABP75962).

Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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100.0%; Pred. No. 1.5e-111;
ive 0; Mismatches 0;
                                                                   ftp.wipo.int/pub/published_pct_sequences
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Matches 252; Conservative
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AAB18461 standard; Protein; 252 AA. (first entry) 15-JAN-2001 AAB18461; AAB18461 RESULT 

A human TANGO 261 polypeptide clone.

TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

Homo sapiens

WO200052022-A1.

08-SEP-2000

01-MAR-2000; 2000WO-US05226.

99US-0122458. 01-MAR-1999; (MILL-) MILLENNIUM PHARM INC

Fraser CC; Barnes TM, Holtzman DA, Sharp JD,

2000-579269/54.

N-PSDB; AAA75163

216, 261, Novel human and murine secreted proteins designated TANGO 216 262, 266 and 267 useful as modulating agents of cellular proc

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AAB18461-63 represent human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular adhesion, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bonchitis, bronchial asthma and bronchisctasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as the example of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treat disorders associated with the ovaries, and mercal ordena, bydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's bisease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                       Disclosure; Page -; 175pp; English.
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for treating cancer
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252 AA; Sequence

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Score 1345; DB 21; Length 252;
Pred. No. 2.3e-111;
1; Mismatches 0; Indels 0;
 Query Match
Best Local Similarity 99.6%;
Matches 251; Conservative
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder;
                                                                                                                                               A human TANGO 261 polypeptide clone.
                                    ż
                                    AAB18462 standard; Protein; 252
                                                                                                            (first entry)
                                                                                                            15-JAN-2001
                                                                       AAB18462;
                 AAB18462
RESULT
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240

ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240

**ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW** 

EEPPPYQCPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180 EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180

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**ESTVSGNGI PEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTI SLSDG** 

1 MAELEFVOIIIIVVVMMVWVVVITCLLSHYKLSARSFISRHSOGRRDDALSSEGCLWPS

1 MAELEFVQIIIIVVVMMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS

9 9

Gaps

; 0

Score 1345; DB 21; Length 252; Pred. No. 2.3e-111; 1; Mismatches 0; Indels 0

99.8%;

Matches 251; Conservative

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Local Similarity

Query Match

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AAB18461-63 represent human TANGO 261 proteins. The specification also describes TANGO 267, TANGO 216, TANGO 267, TANGO 267, TANGO 267, TANGO 267, TANGO 267, TANGO 260 Polypeptides can be used to modulate cellular adhesion, modulate cellular adhesion. The pango proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or cedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder
                                                                                                                                                                                                                                                                                                                                                             Fraser CC;
                                                                                                                                                                                                                                                                                                                                                             Holtzman DA, Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page -; 175pp; English.
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                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                           01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                                                                                                                     99US-0122458
                                                                                                                                                                                                                                                                                                                                                                                                       2000-579269/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA75164.
                                                                                                                                      WO200052022-A1
                                                                                                                                                                                                                                                                     01-MAR-1999;
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             Barnes TM,
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CC corribase and encephalitis, and treat hepatic disorders. It was
                                                                                                                                                                                                                                                                                                                                                                                     cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; plmonary congestion; oedema; emphysema; chronic bronchitals; bronchial asthma; bronchial atthma; bronchial asthma; bronchial asthma; bronchial asthma; bronchial asthma; branchiectasis; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzhaimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes.
                                                                                                                                                                                                                                                                                                                                                                     TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sharp JD, Fraser CC;
                                                                                                                                                                                                                                                                                                                       human TANGO 261 polypeptide clone.
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                                                                                                                                                                              AAB18463 standard; Protein; 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                                                                                                                          (first entry)
                   252
                                                  241 SKEKDKQKGHPL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barnes TM, Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. for treating cancer
                   241 SKEKDKQKGHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-579269/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA75165
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                                                                                                                                                                                                                                                                                                               ESTVSGNGIPEPQVYAPPRPIDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 120
                                                                                                                                                                                                                                                                                                                                                                               EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180
                                                                                                                                                                                                                                                                                                                                                                                                               121 BEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                   ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic, cardiant, cerebroprotective, antiarteriosclerotic, cardiac cell; anti-apoptotic, vascular endothelial cell; cerdiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
                                                                                                                                                                                       1 MAELEFVOIIIIVVVMMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid molecule encoding Mechanically Induced Vascular
Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule encoding Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences AI761441.1, AI594390, NM_004338 and AQ177461. Also included are expression vectors, host
                                                                                                                                        ö
                                                                                         Length 252;
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                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; MIVR-1; Mechanically Induced Vascular; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kennedy SP, Thompson JF,
                                                                                      Score 1345; DB 21;
Pred. No. 2.3e-111;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
(PFIZ ) PFIZER INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU78231 standard; Protein; 287 AA.
created using information provided
                                                                                         99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-2000; 2000US-227159P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEKDKOKGHPL 252
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Landschulz KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-280912/32.
                                                                                                                  Similarity
                                            252 AA
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                                                                                                                                        251;
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                                               Sequence
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                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                      vascular
MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activuth with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VUDD-1, BTG-2 and ITS-11d or its expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and disorders as characterised by increased apoptotic cell-death of vascull endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                     36 ITELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSGGRRREDALSSEGCLWPS
                                                                                                                                                                                                                                                                                                                                                                                                  EEPPPYGGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQOSSGPPSLLEGTRLHHTHIAPLESAAIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW
                                                                                                                                                                                                                                                                                                                   1 MAELEFVQIIIIVVVVMVVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotic; thrombolytic; drug screening; arthritis; inflammation;
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0
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                                                                                                                                                                                                                                               Score 1340; DB 23;
Pred. No. 7.6e-111;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 1857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                  99.4%;
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19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                   250; Conservative
                                                                                                                                                                                  represents human MIVR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKEKDKOKGHPL
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                  287 AA
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19-JUL-2000; 2
03-AUG-2000; 2
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                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 APPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                       Activin/inhibin activity, chemotactic/chemokinctic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 APPRFIDRLAVPFFAQRERFHREQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGNGIPEPQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, MIVR-1; Mechanically Induced Vascular Receptor 1; 
CytoStatic; cardiant; cerebroprotective; antiarteriosclerotic; 
cardiac cell; anti-apoptotic; vascular endothelial cell; 
cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis; 
heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 MAVMAVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGNGIPEPQVY
                                                   Wang
                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                   Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Mechanically Induced Vascular Receptor 1, MIVR-1.
                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.1%; Score 1282; DB 22;
100.0%; Pred. No. 8.5e-106;
iive 0; Mismatches 0;
                                                 Chen R, Ma Y,
Xu C, Xue AJ,
S, Drmanac RT;
                                                                                                                                                                                                                               Example 3; SEQ ID NO 1857; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU78236 standard; Protein; 274
                                                 Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 237; Conservative
                                                                                                                      2001-442253/47.
                                                Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 AA;
                HYSEQ INC
                                                                                                                    WPI; 2001-442253/
N-PSDB; AAI57868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196
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                                                   ΥŢ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                (HXSE-)
                                                   Tang
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요
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musculus

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peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                         chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, us such as central nervous system injuries
              polypeptide SEQ ID NO 5429
                                                                                                                                                                                                                                                                                      26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAI59654
                                                                                                                                                                                                                 WO200153312-A1
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2000;
                                                                                                                                                                                                                                                                                                                          21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                               09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                           25-APR-2000;
                                                                                                                                                                                                                                                   26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 207;
                                                                                                                                              leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p, q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YT,
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Wang
Zhao
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule encoding a Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having cardival anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences A1761441.1, A1594390.

WM 004338 and AQ177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its modulated and thereby identifying a modulator activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and calsorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 ESTVSG-GMPEPQVYAPPRPTDRLAVPPFIQRS---RFQPTYPYLQHEIALPPTISLSDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 ITELEFVQIVVIVVWMWWWWWITCLLSHYKLSARSFISRHSQARRDDGLSSEGCLWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 EEPPPYQGPCTLQLRDPEQQLELMRESVRAPPNRTIFDSDLIDSTMLGGPCPPSSNSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 ATCYSSGGRWEGPPPTYSEVIGHYPGSSFQHQQSNGPSSLLEGTRLHHSHIAPLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAELEFVQIIIIVVVMMVWVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCYGSGGRMEGPPPTYSEVIGHYPGSSPQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                Turi
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                                                                                                                                                                                                Thompson JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 1172.5; DB : 88.1%; Pred. No. 5.4e-96; ive 11; Mismatches 10
                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 100-101; 105pp; English
                                                                                                                                        BGHM ) BRIGHAM & WOMENS HOSPITAL INC
PFIZ ) PFIZER INC.
                                                                                                                                                                                                Kennedy SP,
                                                                   21-AUG-2001; 2001WO-US26089.
                                                                                                        22-AUG-2000; 2000US-227159P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
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Best Local Similarity 88.15
Watches 222; Conservative
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263 NKEKEKQKGHPL 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents mouse MIVR-1
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                                                                                                                                                                                                Landschulz
                                                                                                                                                                                                                                    WPI; 2002-280912/32
                                                                                                                                                             PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AA;
                                                                                                                                                                                                                                                   N-PSDB; ABK12142
WO200216416-A2
                                   28-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                Lee RT,
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AAM40498
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Wang

Ren F, W. Zhang J;

Qian XB, Yang Y,

ien R, Ma Y, ( u C, Xue AJ, Drmanac RT;

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Liu C, A Wang Z, W Zhou P,

Goodrich R, Asundi V, Wehrman T,

Chen R,

2000US-0598042.

2000US-0552317

2000US-0653450

2000US-0662191. 2000US-0693036. 2000US-0727344. useful for treating disorders

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                                                                               the encoded polypeptides (AAAA213) with noctropic, the encoded polypeptides (AAAA213) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, encropathy and localised neuropathies and central nervous system diseases, encode as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activities such as: Immune system suppression, Activinihibin activity, chemotactic/chemokinetic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 RLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGP<u>PSL</u>LEGTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                               assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.N.S disorders.
Note: The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1133; DB 22;
Pred. No. 1.2e-92;
0; Mismatches 0;
Example 2; SEQ ID NO 5429; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.1%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification
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AAM40498 standard; Protein; 207

(first entry)

22-OCT-2001 AAM40498;

HXXXH

b-17.rag

252 181 LHHTHIAPLESAAIWSKEKDKOKGHPL 226 LHHTHIAPLESAAIWSKEKDKOKGHPL 121 셤 ઠે 원

AAB18450

AAB18450 standard; Protein; 217 AA

AAB18450;

(first entry) 15-JAN-2001

murine TANGO 261 polypeptide.

TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
collular proliferation; cellular differentiation; cellular adhesion;
on Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atlectashs; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
ardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease, cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

Mus sp.

WO200052022-A1.

08-SEP-2000

01-MAR-2000; 2000WO-US05226.

99US-0122458. 01-MAR-1999; (MILL-) MILLENNIUM PHARM INC.

Fraser CC; Sharp JD, Barnes TM, Holtzman DA,

WPI; 2000-579269/54. N-PSDB; AAA75152.

Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -

Claim 8; Fig 6A-B; 175pp; English.

disorders, atelectasis, pulmorary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, The present sequence represents a murine TANGO 261 polypeptide. The specification also describes TANGO 266, TANGO 216, TANGO 267. The TANGO 267, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficient and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and 

146 ||| || PPFIQRS---RFQPTYPYLQHEIALPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRE 116 SVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPG 206 SVRAPPNRTIFDSDLIDSTMLGGPCPPSSNSGISATCYSSGGRMEGPPPTYSEVIGHYPG 176 59 PPFAQRERPHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRE 1 LSHYKLSARSFISRHSQARRADDGLSSEGCIMPSESTVSG-GMPEPQVYAPPRPTDRLAV 27 LSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAV Gaps brain cancers, hydrocephalus and encephalitis, and treat hepatic و . Length 217; SSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252 Score 1066.5; DB 21; Lengt Pred. No. 1.1e-86; ; Mismatches 9; Indels SSFQHQQSNGPSSLLEGTRLHHSHIAPLE-----NKEKEKQKGHPL 7; 79.18; 88.9%; Matches 201; Conservative Query Match Best Local Similarity 217 AA; disorders. 147 87 117 9 207 177 Sequence ន្តដ្ឋនូ ò g ઠે a ò ద ò 셤

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ABG77052 standard; Protein; 241 AA. RESULT 13 ABG77052

ABG77052;

05-NOV-2002 (first entry)

Prostate specific protein #22.

Human, prostate specific nucleic acid, PSNA, prostate cancer, cytostatic, non-cancerous prostate disease, PSP, vaccine, prostate specific protein, metastasis.

Homo sapiens.

WO200242776-A2

30-MAY-2002

01-NOV-2001; 2001WO-US45654.

01-NOV-2000; 2000US-244782P

(DIAD-) DIADEXUS INC.

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Liu

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Chen

Recipon H,

Sun Y,

WPI; 2002-490217/52.

and New polypeptide useful for diagnosing and monitoring the presence metastases of prostate cancer in a patient and as a component in databases for search analysis as well as in sequence analysis algorithms

Claim11; Page 213-214; 242pp; English.

The invention relates to an isolated polypeptide comprising a sequence with 60 % identity to one of prostate specific protein (PSP) sequences, or comprising an amino acid sequence encoded by one of 136 nucleotide prostate specific nucleic acids sequences, PSNA, (or a sequence that hybridises to it or is 60% identical to it), given in the specification. Also included are a vector comprising the polynucleotide, a host cell acomprising the vector, an antibody specific for the PSP proteins and a vaccine comprising the protein or polynucleotide. The PSP and PSNA are useful for diagnosing and monitoring the presence and metastasses of prostate cancer in a patient. The PSNA is useful for determining the 

O Page Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -

English.

-; 175pp;

Disclosure; Page

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1;
the level PSNA in a sample. An antibody to the PSP is useful for determining the presence of prostate specific protein in a sample, and for treating a patient with prostate cancer, which induces an immune response against the prostate cancer cell expressing the nucleic acid or polypeptide and a kit is useful for detecting a risk of cancer or presence of cancer in a patient. PSNA is useful as hybridisation probes to detect, characterise and quantify hybridising nucleic acids from both genomic and transcript-derived nucleic acid samples and also in microarrays. Sequences of PSP and PSNA are useful as components in databases for search analysis as well as in sequence analysis algorithms. PSNA is useful to drive in vivo expression of PSP. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 267;

cellular proliferation; cellular differentiation; cellular adhesion;

von Willebrand factor-associated disorder; cell trafficking; cancer;

hematopoietic associated disease; atlectasis; pulmonary congestion;

oedema; emphysema; chronic bronchitis; bronchial asthma; bronchial

intestinal disorder; spleen associated disease; renal disorder;

ardiovascular disorder; ischemic heart disease; hydrocephalus;

brain herniation; iatrogenic disease; inflammation; meningitis;

Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;

multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                   1 EGCLWPSESTVSGNGIPECPCCWDPPCRRSSAPCPAGSSPALCSLHTGARTLPLFGGGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 QLRDPEQQLELNRESVRAPPNRT1FDSDLMDSARLGGPCPPSSNSG1SATCYGSGGRMEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTL
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60 PPFIQRS---RFQPTYPYLQHEIALPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRE 116
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                                                                                                 1 LSHYKLSARSFISRHSQARRRDDGLSSDGCLWPSESTVSG-GMPEPQVYAPPRPTDRLAV
                                                                                                                                                     PPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRE
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                                                                           27 LSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAV
Score 1063.5; DB 21; Length 217; Pred. No. 1.9e-86; 8; Mismatches 9; Indels 9;
                                                                                                                                                                                                                                                                                                        SSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
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N-PSDB;

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Mus sp.

01-MAR-1999;

AAB18464-66 represent murine TANGO 261 proteins. The specification also describes TANGO 265, TANGO 262, and TANGO 267. The TANGO 260 to properties can be used to modulate cellular adhesion, modulate cellular adhesion. The TANGO collular adhesion and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as intending the cells and to treat bone and/or and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders, note: the present sequence does not appear in the specification; it was created using information provided. 217 AA; Sequence Fraser CC; Sharp JD, (MILL-) MILLENNIUM PHARM INC. 01-MAR-2000; 2000WO-US05226 99US-0122458 Barnes TM, Holtzman DA,

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Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, hydrocephalus, encephalitis, hepatic disorder

Mus sp.

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01-MAR-2000; 2000WO-US05226.

99US-0122458 01-MAR-1999; (MILL-) MILLENNIUM PHARM INC

Fraser CC; Sharp JD, Barnes TM, Holtzman DA,

WPI; 2000-579269/54. N-PSDB; AAA75167.

Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes. e.g. for treating cancer -

Disclosure; Page -; 175pp; English.

AAB18464-66 represent murine TANGO 261 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 200 cloppyptides can be used to omodulate cellular spoiliferation, modulate cellular adhesion, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficting and/or migration, adollate cellular interactions, modulate cell adhesion in proliferation, adollate cellular interactions, and cell function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated disease, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disorates, treat cardiovascular disorders such as ischemic heart disorate disease with the ovaries, and cerebral oedema, cartilage associated disease with the ovaries, and cerebral cancerial and viral meningitis, Alzheimer's Disease, inflammations, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, and treat hepatic disease, inflammations, bacterial and viral meningitis, and treat hepatic disease, inflammations, brain disease, multiple sclerosis, brain cancers, note: the present sequence does not appear in the specification; it was note: the present sequence does not appear in the specification; it was created using information provided. 

217 AA; Sequence

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Best Local Similarity 88.5%; Pred. No. 1.9e-86;
Matches 200; Conservative 8; Mismatches 9; Indels 86 27 LSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAV

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## ALIGNMENTS

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SESTWSGNGT PEPQYYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISL
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NSGISATCYGSGGRWEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAP
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Jene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_cref="taxon:9606"
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/tissue type="Kidney, renal cell adenocarcinoma"
/clone_lib="NH10B-R"
/lab host="Netcor: pOTB7"
                                                                                                                     CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
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/codon_start=1
/product="Unknown (protein for MGC:20374)"
/protein_id="AAH15918.1"
/db_xref="G1:16198475"
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                                                     URL: http://mgc.nci.nih.gov
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100.0%; Pred. No. 0;
iive 0; Mismatches 0
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                                               NIH-MGC Project URL: http://m
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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AF224278
Homo sapiens PMEPA1 protein (PMEPA1) mRNA, complete cds.
AF224278
AF224278.1 GI:9255808
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1141)
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A novel androgen-regulated gene, PMEPA1, located on chromosome 20q13 exhibits high level expression in prostate Genomics 66 (3), 257-263 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Segawa, T., Sesterhenn, I.A., McLeod, D.G.,
                                                      690 GCCACTACCCGGGGTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG
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Moul,J.W. and Srivastava,S.
Direct Submission
Submitted (12-JAN-2000) CPDR, US
Rockville, MD 20852, USA
Location/Qualifiers
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Homo sapiens PMEPA1 variant A protein mRNA, complete cds. AY128643 AY128643.1 GI:22121998
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NSGISATCYSGGGRWEGPPPTYSEVIGHYPGSSFQHQQSSGPPBLLEGTRLHHHIAP
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Wilson,J.K.V., Lu,S., Nosrati,A., Swinler,S., Beard,L.,
Lutterbaugh,J.D., Willis,J., Platzer,P. and Markowitz,S.
Direct Submission
Submitted (03-JUL-2002) Department of Medicine, Case Western
Reserve University/Howard Hughes Medical Institute, 11001 Cedar
Ave., Cleveland, OH 44106, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          976 CACCTCCCTGTGTATAAATATTTACATGTGATGTCTGGTCTGGTCTGATGCACAAGCTAAGAGA
                                                                                                                                             TAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGG
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/product="PMEPA1 variant
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/chromosome="20"
/map="20q13.31-13.33"
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VERSION
KEYWORDS
SOURCE
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PUBMED
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MARLEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQG
RRREDALSSEGCLWPSESTVGGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTV
PYLQHEIDLPPTISLSDGEEPPPYGGPCTLQLRDFEQQLELNRESVTAPPNRTIFDSD
LMDSALLGGPPPSSNSGISATCYGGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPP
SLEGTRLHHTHIAPHLSAALWSKEKDKQKGHPL"
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/db_xref="G1:9255809"
      sapiens
/organism="Homo sapiens
mol_type="msNa"
db_xref="taxon:9606"
/chromosome="20"
/map="20q13.31-13.33"
/cell_line="LNCaP"
                                                                                                                                           gene="PMEPA1"
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/ Droduct = "6TAG1/PMEPA1"

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/ protein id="AAL16781.1"

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/ branslat ion="WHRIMGYNSTAAAAAQPNVSCTCNCKRSLFQSMEITELEFVQ1

IIIVVVMMVNVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGN

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1 (bases I to 48139)

Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
Characterization of a novel gene, STAGI/PMEPAI, upregulated in renal cell carcinoma and other solid tumors
Mol. Carcinog. 32 (1), 44-53 (2001)
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Rae,F.K., Hopper,J.D., Nicol,D.L. and Clements,J.A.
Direct Submission
Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane,
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1. 04839
| Caganism="Homo sapiens" |
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| db xref="taxon:9606" |
| chromosome="20" |
| map="20q13.2-q13.33" |
| 321. 1184 |
| /note="unknown function"
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YQGPCTLQLARDEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATC
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THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. Location/Qualifiers
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/db_xref="taxon:9606"
/13. .1276
/note="unnamed protein product"
/codon_start=1
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Turi, T.G.
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YQGPCTLQLADPRQQLELNESSYRAPPNRTIFDSDLWDSARLGGPPCPPSSNSGISATC
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                                                                                                                 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.

Turi, T.G.

Diagnosis and treatment of cardiovascular conditions

Patent: WO 0216416-A 3 28-FEB-2002;

THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER INC.
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Pred. No. 0;
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Homo sapiens solid tumor-associated 1 protein (STAG1/PMEPA1) gene,
complete cds.
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YQGPCTLQLRDDPGQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATC
YGGSGRMEGPPPTYSEVIGHYPGSSPOHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
Direct Submission
Submitted (13-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane,
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Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
Identification and characterization of a novel gene,
up-regulated in renal cell carcinoma and other solid
Unpublished
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/gene="STAG1/PMEPA1"
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CB10 1SA, UK. E-mai requests: clonereque on Dec 5, 2000 this During sequence as Mere differences a together with a not variation annotation corresponding to the collowing abbre numbers given in the following abbre numbers given in the Em:, EMBL; Sw:, SWI	on the WORNPEP data, http://www.aanger.a was generated from chromesome 20, cons Mapping Group. Fur http://www.sanger.a This sequence is th end of clone RPS-10	right end of clone RP4-718J7 is from t Pieter de Jong. For http://www.chori.or VECTOR: pCYPAC2	This sequence was f regions were either chemistry or covere 30); an attempt was	as compressions and one plasmid subclon assembly was confirmed	Source Location Source   1. 130432	/chromosom /map="q13. /clone="RP	repeat_region 319478 /note="5 c repeat_region 370463	repeat_region /ioce=2 c /note=4 c repeat_region /07. 812 /note==53	repeat_region 9672752 /note="893 repeat_region 9822730 /note="33 repeat_region 1177182 /note="4 repeat_region 1204137 repeat_region 1204137	/note="28 repeat_region 1675271 /note="18 repeat_region 1843234 /note="9 c	repeat_region 2028. 263 /note="11 repeat_region 2087. 225 /note="3"	repeat_region 2228249 /note="5 c repeat_region 2583271 /note="2 c
372 AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCGTACCTGCAGCACGAGATCGACC 431		AGGGGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCAGC	732 ACCAGCAGAGCAGTGGGCCGCCTCCTTGCTGGAGGGAACCCGGCTCCACCACACACA	792 TCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAACAGAAAGACACC 851 	852 CTCTCTAGGGTCCCCAGGGGGCCCGGGCTGCGTAGGTGAAAAGGCAGAACACTC 911 	912 CGCGCTTCTTAGAAGAGAGTGAGAAGGCGGGGGGGCGCACCAACGCATCGTGGCC 971	972 CTCCCCTCCCACTCCCTGTGTATAAATATTTACATGTGATGTCTGGTCTGAATGCACAA 1031 	1032 GCTAAGAGCTTGCAAAAAAAA 1057 	8 7/c FION	transmembrane protein (PMEPA1), two putative novel genes, a CpG island, ESTB, STSB and GSSB, complete sequence. SION AL035541 DN AL035541.15 GI:11546043 RDS HTG; CpG island; DLM-1; macrophage protein; PCK1; phosphoenolpyruvate carboxykinase; PMEPA1; Transmembrane	_	1 (bases 1 to 130435) Sehra, H. Direct Submission Submitted (23-FEB-2001) Sanger
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erequest@sanger.ac.uk this sequence version replaced gi:10198628.

this sequence version replaced gi:10198628.

e assembly data is compared from overlapping clones.

ces are found these are annotated as variations
a note of the overlapping clone name. Note that the
tation may not be found in the sequence submission
to the overlapping clone, as we submit sequences with
verlap as described above.

abbreviations are used to associate primary accession
in the feature table with their source databases:

'SWISSPROT' Tr:, TREMBL; Wp:, WORMPEP; Information
database can be found at
ger.ac.uk/Projects/Celegans/wormpep This sequence
from part of bacterial clone contigs of human
constructed by the Sanger Centre Chromosome 20
Further information can be found at
Further information can be found at
Further information can be found at
Further sequence.

18-100786 is at 71437 in this sequence. The true
10ne RP4-579F20 is at 43945 in this sequence.

10 For further decails see
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enquiries: humquery@sanger.ac.uk Clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies 57 mer 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    copies 54 mer 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rg/bacpac/home.htm
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>e="genomic DNA"
:="taxon:9606"
some="20"
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RP4-718J7"
ib="RPCI-4"
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copies 67 mer 82% conserved"

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.799. .3896
note="Charliel repeat: matches 681. .781 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L1MD2 repeat: matches 6032. .6331 of consensus"
378. .3426
note="LiMB4 repeat: matches 6088. .6136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Alujb repeat: matches 188. .300 of consensus" 10563. .10573
note="Alujb repeat: matches 1. .308 of consensus" 10658. .10753
note="L2 repeat: matches 2647. .2749 of consensus" 1816. .12380
                                                                                                                                                                                                                                                                                                                                                                         863. .9217
note="MLT1D repeat: matches 105. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                              note="FLAM_C repeat: matches 1. .132 of consensus"
                                                                                                                                                                                                                                                           952. .7021 | note="L2 repeat: matches 2637. .2705 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .580 of consensus"
                                                                                            consensus
                                                                                                                                                                                                                                                                                                358. 7671
note="Alusx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 86. .211 of consensus" 18312. .18438 /note="MIR repeat: matches 138. .250 of consensus" 18585. .18776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluSx repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                         .218 of consensus"
                                                                                                                                                                                                                                                                                                                                     3521. .8554
note="nlu repeat: matches 1. .34 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="14 copies 6 mer cacaca 82% conserved"
5029. 15108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="22 copies 6 mer ctctct 67% conserved"
3586. .13717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οĘ
                                                                                                              7197. .5988

Copies 32 mer 86% conserved"

8855. .5978

Mote="31 copies 4 mer gcac 61% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="34 copies 4 mer cttt 77% conserved"
complement(13622, .14142)
/note="match: GSS: Em:AQ592603"
14313, .14437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="20 copies 4 mer acac 83% conserved" 5273. .15399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "note="66 copies 2 mer tc 68% conserved"
3588. 13715
"note="4 copies 32 mer 78% conserved"
3589. 13724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="45 copies 2 mer ac 80% conserved"
5026. .15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="LTR16C repeat: matches 257. .386
                                                                         331. .5793
note="MLT1B repeat: matches 14. .466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="3 copies 56 mer 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="3 copies 32 mer 79% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR19B repeat: matches 1.
2519. .12813
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8049. .18169
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                                                                                                                                                                                   474. .6591
note="MIR repeat: matches 91.
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128263 CCCTCCAGCTTCGGGACCCCCAGCAGCTGGAACTGAACCGGGAGTCGGTGGCGCGCAC 128204
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note="FLAM_C repeat: matches 1. .127 of consensus" 31203. .31356 /note="LIMBS repeat: matches 6015. .6176 of consensus" 32224. .32522.
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/note="L2 repeat: matches 2661. .2739 of consensus"
/7823. .28041
/20129. .28259
                                                                                                                                                                                               11667. .21775

/note="MIR repeat: matches 73. .192 of consensus"

/note="2.2546"

24257. .24591

/note="L2 repeat: matches 2336. .2710 of consensus

25580. .25611

/note="16 copies 2 mer tc 87% conserved"
   consensus,
                                                                                                                                                                                                                                                                                                                6333. .26643
note="Aluy repeat: matches 1. .310 of consensus"
7603. .27684
            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 130435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
note="MER20 repeat: matches 7. .217 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 1. .298 of
                                                                                                                                    complement (21278. .21663)
//note="match: 6SS: Em.AQ136459"
complement (21392. .21672)
/note="match: GSS: Em.AQ892114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 65.5%; Score 695; DB Best Local Similarity 99.9%; Pred. No. 0; Matches 745; Conservative 0; Mismatches
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1187 GGGGCCGCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTTCCAGCA 1246
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                             Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Dramanc, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B. Human genes and gene expression products
Patent: WO 0102568-A 1739 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGGGGCGGAGGAGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAG
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                             CCAGCAGAGCAGTGGGCCGCCCTTCCTTGGAGGGGACCCGGCTCCACCACACAT
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larity 99.8%; Pred. No. 1.5e-171;
Conservative 0; Mismatches 1; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
_159 c 115 g 53
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                                                                    CGCGCTTCTTAGAAGAGGAGTGAGAGGAAGGCGGGGGGCGCAGCAACGCATCGTGTGGCC
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Pred. No. 7.2e-255;
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1. 1583
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.8%; Pred. No. 7.2e
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Turi,T.G.
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Sequence 14 from Patent WO0216416.
AX392430
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/db_xref="taxon:9606"
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GGGCGCAGCAACGCATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTATAAATATTACA 1006
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Human DNA linear PRI 24-FEB-200

Human DNA sequence from clone RPS-1059L7 on chromosome

20q13.2-13.33 Contains the 5' end of the TMEPAI (PMEPAI) gene
encoding an androgen induced 1b transmembrane protein, ESTB, STSB,

AL121913

AL121913

HUMO CpG islands, complete sequence.

HTG; CpG island; PMEPAI; TMEPAI; transmembrane protein.

HTG; CpG island; PMEPAI; TMEPAI; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                         587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGGA-G 766
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 150224)
                                                                                                                                                                                                                                                                                                                                                                                                                  467 ATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCACGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 GCGTAGGTGAAAAGGCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAGGAAGGCGGG
                                                                                                                                                                                                                                                                                                       CCCCACCCTACCAGGCCCCTGCACCCTCCAGGCTCCGGGACCCCGAGCAGCAGCTGGAAC
                                                                                                                                                                                                                                                                                                                                                 587 CCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                              TGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGG
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                        ; PFIZER INC. (US)
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Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambrids
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                                                                                                                                                        others
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                        (ns)
                                                                                                                                                                                                                  29.5%; Score 313; DB 6; 1
llarity 99.3%; Pred. No. 3.6e-152;
Conservative 0; Mismatches 3;
Patent: WO 0216416-A 14 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
Location/Qualifiers
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                                                                                                                                                          149
                                                                1. 693
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
a 205 c 237 g 149
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                                                                                                                                                                                                                                                            Matches 583;
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4.oligo.rge

/evidence=not\_experimental /product="dJ1059L7.1.1 (androgen induced type 1b transmembrane protein (PMEPA1), isoform 1)" /protein id="CAB88144.1" /db xref="G1:7619746" /db xref="SPTREMBL.20PUTS" /tb xref="SPTREMBL.20PUTS" /translation="WGVNSTRAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQIIIIV note="Charlie4 repeat: matches 39. .146 of consensus" note="L2 repeat: matches 2290. .2705 of consensus" note="MER20 repeat: matches 1. .187 of consensus" 224. .5282 note="MIR repeat: matches 94. .154 of consensus" note="MIR repeat: matches 11. .196 of consensus" consensus, repeat: matches 81. .239 of consensus" /evidence=not\_experimental complement(join(<2445. .2599,52376. .52472)) 2538. .2567 /note="10 copies 3 mer cac 90% conserved" note="19 copies 2 mer tt 81% conserved"
792. .5001
note="3 copies 70 mer 82% conserved"
002. .5190
note="MSR20 repeat: matches 1. .200 of note="23 copies 2 mer at 76% conserved" note="AluSx repeat: matches 1. .311 of 8103. .8205 /note="MIR repeat: matches 48. .161 of complement(8858. .9277) 394. 3893 note='25 copies 20 mer 59% conserved" 1407. 3892 3553. .3932 Mote="10 copies 38 mer 64% conserved" 1573. .3697 note="5 copies 25 mer 76% conserved" note="19 copies 28 mer 61% conserved" 394. .3893 407 .3892 note="27 copies 18 mer 58% conserved" copies 36 mer 58% conserved" -"3 copies 25 mer 92% conserved" .3921 "5 copies 25 mer 76% conserved" .3921 note="3 copies 37 mer 83% conserved" copies 70 mer 62% conserved" /note="continues in dJ718J7 (AL015541 match: proteins: Tr:015166 Tr:015168" /codon\_start=1 copies 22 mer 64% conserved" 3128. .3606 /note="match: GSS: Em:AQ059507" note="match: GSS: Em:AQ881699" note="match: GSS: Em:AQ565377" note="match: GSS: Em:AQ757992" /evidence=not\_experimental note="CpG island" gene="TMEPAI" 0140 1175. .11343 .12362 .14493 .12037 3421. .3910 /note="7 cop: 3473. .3904 /note="12 cor . 9382 .9861 032. .4069 214. .3324 339. .3413 note="MIR note="8 note="3 repeat\_region misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature CDS corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. 'translation="MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQG" requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:7007305.
On Muring sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission /product="dJ1059L7.1.1 (androgen induced type 1b transmembrane protein (PMEPA1), isoform 1)" /note="match: cDNAs: Em:AF009426 Em:AF009427 Em:AF009425 2076. 2155 /note="12 repeat: matches 2616. .2707 of consensus" E-mail enquiries: humquery@sanger.ac.uk Clone 'note="MIR repeat: matches 71. .145 of consensus" .165 of consensus" /evidence=not\_experimental /product="dJ1059L7.1.2 (androgen induced type 1b transmembrane protein (PMEPA1), isoform 2)" /protein id=10AC32887.1" /db\_xref="GI:13160408" /product="dJ1059L7.1.2 (androgen induced type 1b transmembrane protein (PMEPA1), isoform 2)"
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match: ESTs: Em:AA088767" match: ESTs: Em:AA249792 Em:AI594390 Em:AA128075 complement (join (<2445. .2599,53362. .53425)) /gene="TMEPAI" /evidence=not\_experimental complement(join(<2445. .2599,53362. .53365)) complement(join(<2445. .2599,52376. .52477)) 'note="continues in dJ718J7 (AL035541)" 1509. .1628 /note="MIR repeat: matches 46. nttp://www.chori.org/bacpac/home.htm complement (2445. .53425) /gene="TMEPAI" 'organism="Homo sapiens" /mol\_type="genomic\_DN /db\_xref="taxon:9606" /chromosome="20" Location/Qualifiers /map="q13.2-13.33" /clone="RP5-1059L7" /clone\_lib="RPCI-5" 283. .355 gene="TMEPAI" codon start=1 gene="TMEPAI" Em: AF009424 further details see VECTOR: pCYPAC2 repeat\_region repeat\_region repeat\_region gene mRNA mRNA FEATURES CDS COMMENT

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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, and Biotechnology Center, National Institute of Technology and HRI, and Biotechnology Center, National Institute of Technology and HRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="NTZRI200689"
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/cell Line="NTZ"
/cell Line="NTZ"
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/clone line="NTZ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGGTTCAGTGGGCCATGATCCCCGGAGCTGC 322
                                                                                                                                         1 (bases 1 to 2570)
18ogal, T., Otsuki, T. and Sugiyama, T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
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Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Soblima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 79; DB 9; Lt
100.0%; Pred. No. 1.4e-29;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 bp C
Sequence 495 from Patent W00151670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
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Best Local Similarity 100.C
Matches 79; Conservative
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                                                                                           TITLE
JOURNAL
REFERENCE
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2540 GTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCAC 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="LiMb1 repeat: matches 6102. .6221 of consensus"
24752. .25042
//note="Li2 repeat: matches 2386. .2709 of consensus"
52508. .25295
//note="Mix repeat: matches 61. .155 of consensus"
86450. .26485
                                                                                                                                                                                                                                                                                                                                                              /noce="L2 repeat: matches 2581. .2750 of consensus"
20530. .21282
/note="L1MD2 repeat: matches 5595. .6341 of consensus"
21980. .22192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 GCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                note="L2 repeat: matches 2358. .2411 of consensus" 0264. .20432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2562 of consensus"
                                                                       note="MLT1A2 repeat: matches 1. .374 of consensus"
7647. .17703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 117. 218 of consensus" 2321. .23438
/note="MER20 repeat: matches 3. .218 of consensus" 24439. .22512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .257 of consensus"
                                                                                                                                                                                                                       note="MIR repeat: matches 107. .243 of consensus"
                                                                                                                                                                                                                                                                       .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 55. .190 of consensus" 29550. .29728
/note="MIR repeat: matches 69. .248 of consensus"
15690. .15935
Thote="MIR repeat: matches 7. .254 of consensus"
16989. .17387
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
                                                                                                                    note="L2 repeat: matches 2679.
17699. 18179
note="match: GSS: Em:AQ703107"
17902. 18039
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23102, ,23203
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note="MIR repeat: matches 35.
9954. .20005
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                                                                                                                                                misc_feature
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PAT 29-AUG-2001

linear

/note="1 of 2 allelic variants (496 is other entry) Accession number cg42747251"

misc\_feature

Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 14 AK056098/c DEFINITION

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9

Gaps

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Length 2570;

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12 a BASE COUNT ORIGIN

0; Gaps Ouery Match 4.8%; Score 51; DB 6; Length 51; Best Local Similarity 100.0%; Pred. No. 7.4e-15; Matches 51; Conservative 0; Mismatches 0; Indels

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Search completed: December 8, 2003, 05:33:47 Job time : 4149 secs

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December 8, 2003, 02:02:00 ; Search time 344 Seconds (without alignments) 8325.883 Million cell updates/sec
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| SIDSI/Gogdata/geneseqf/geneseqn-embl/NA1981.DAT:*
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| SIDSI/gogdata/geneseq/geneseqn-embl/NA1985.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2552756 seqs, 1349719017 residues
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	Description	Sequence encoding	Human secretory po	cDNA encoding a hu	cDNA clone encodin	Prostate cancer-as	cDNA clone encodin	cDNA clone encodin	Human polynucleoti
COLUMNIES	ID	•	ABZ36103	AAA75151	AAA75163	ABK92120	AAA75164	AAA75165	AA157868
	ОВ	21	25	21	21	24	21	21	22
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di	Query Match	100.0	99.5	90.6	89.7	87.3	85.8	85.8	84.0
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ABK12137 AAI59654 ABS61424 ABZ84732 AAF65983 AAZ52964	AAA1265 AAS84502 AAS84503 ABT10027 ABN40872 AAH89714 ABK12142 AAA75152 AAA75166	AAA71168 ABA50210 ABA50210 ABA5522 ABA5522 AAK16592 AAK16592 AAK16592 AAK16592 AAK16592 AAK16592 AAK16592 AAK16592 AAK16592 ABA5523	ABA55612 ABA25310 AAK03841 AAK29307 AAI13901 AAI35267 AAI03769	rd; DNA; 1061 BP.  irst entry)  ng human neuron-associated ed protein; NEUAP; neurolo ovascular disease; stroke; ease; Pick's disease; Hun nson's disease; Hun son's disease; mixek turu; Crentzfeldt-Jakob di. muscular dystrophy; centri ous system; PNS; myopathy; ous system; PNS; myopathy; is; arteriosclerosis; athe titis; mixed connective ti paroxygmal nocturnal haemo ase; inflammation; acquirec disease; adult respirator; sing spondylitis; amyloido; trauma; human; ds.  Location/Qualifiers 101.859	uron associ
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98US-0210083. 98US-9123456. 99US-0119365. 99WO-US30408 99US-0124687 (INCY-) INCYTE PHARM INC WO200034477-A2 11-DEC-1998; 11-DEC-1998; 16-MAR-1999; 10-DEC-1999; 15-JUN-2000. Tang YT, Lu DAM, 

Yang Hillman JL, Lal P, Au-young J, Baughn MR, Yue H, Ba Azimzai Y;

۵,

2000-423423/36. P-PSDB; AAB01388 New human neuron-associated proteins and polynucleotides encoding them, useful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders

Claim 9; Page 136; 145pp; English

Human neuron-associated proteins (NEUAP) can be used for for treating or preventing a disorder associated with decreased treating or preventing a disorder associated with decreased cypression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NEUAP. Their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia and experimenting diseases, but information's disease, neurological disorder such as epilepsy, ischemic diseases including kuru, Creutzfeldt-Jakob disease, nutritional and diseases including kuru, Creutzfeldt-Jakob disease, nutritional and evelopmental disorders of the central nervous system cerebral conternation of the central nervous system disorders, palsy, neuroskeletal disorders, palnal cord diseases, muscular dystrophy and cother neuromuscular disorders, paritheral nervous system disorders, inherited, metabolic, endocrine, and scritophrenic disorders, antender disorders, conternative disorders under as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal connective disorder such as actinic keratosis, arteriosclerosis, bursitis, cirrhosis, paroxysmal nocturnal connective disorder such as acquired immunodeficiency syndrome (ALDS), Addison, disorders under as acquired immunodeficiency syndrome (ALDS), Addison, complications of cancers of the adrenal gland, bladder, bone marrow, brain, breast, cervix, and an autoimmune, and cancers of the adrenal gland, werner syndrome complications of cancer, hemodialysis, and extracorporeal circulation, infections, and trauma. This sequence was given the Incyte ID no. 1971288CBI.

Sequence 1061 BP; 225 A; 342 C; 326 G; 168 T; 0 other;

Query Match

DB 21; Length 1061;

ö 9 9 TCCTCCTTGGTTCGGGTGAAAGCGCTTGGGGGTTCAGTGGGCCATGATCCCCGAGCTGC 1 TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGTTCAGTGGGCCATGATCCCCGAGCTGC Gaps ; Indels , 0 100.0%; Score 1061; 100.0%; Pred. No. 0; 0; Mismatches Conservative Best Local Similarity Matches 1061; Conserv ð g

Human secretory polynucleotide SPTM SEQ ID NO 267.

(first entry)

10-FEB-2003

ABZ36103;

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61 TGGAGAACTGAAGGCGGACGGTCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGT

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ATCGTGTGGCCCTCCCCTCCCCTCTCTGTGTAAATATTTACATGTGATGTCTGGTC 1020 300 900 TCAGATCATCATCATCGTGGTGATGATGGTGATGGTGGTGGTGGTGATCACGTGCCTGCT 180 240 240 300 360 420 420 480 480 540 540 600 900 9 99 720 720 780 780 840 840 900 960 960 CGGGCGCATGGAGGGCCGCCCCCACCTACAGCGAGGTCATCGGCCACTACCGGGGTC 841 GAAAGGACACCTTCTTAGGGTCCCCAGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAG gaeccactacaaectercrecaceerccrrcarcaecceecacaeccaeeegeegaeae agaagargcccrgrccrcagaaggargccrgrgggcccrcggagagcacagrgrcaggcaa GCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCA CGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCTACCA GGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTC GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT GGGCGCCCCTGCCCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAGCGG GGGGGCCCCTGCCCCCCCCGGGGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAGCGG CTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCA CCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAAGGATAAACA ccacacacacarcececerragagagegecacearcregagegagagagagagaraaaca GAAAGGACACCCTCTAGGGTCCCCAGGGGGGGCGGGGTGGGGCTGCGTAGGTGAAAAG GCAGAACACTCCGCGCTTCTTAGAAGAGGAGGAGGAAGGCGGGGGGCGCAACGC GAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCCAGGGGGCGGAGGAG AGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAA GCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCA GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT CGGGCGCATGGAGGGGCCGCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC CTCCTTCCAGCACCAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCA 1061 BP. ABZ36103 standard; cDNA; 1334 1021 721 781 241 241 361 541 961 1021 301 601 781 181 181 301 361 421 421 481 481 541 601 661 661 721 841 901 RESULT 2 ABZ36103 g 원 셤 a 셤 셤 ò 원 ð В ò g ò g à 셤 ò 셤 XEXEXEX 셤 ò g ð à 8 ò ò ò 8 셤 ð

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Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; neurolpetic; antisonvulsant; cytostatic, antisparkinsonian; anxiolytic; secretory polynucleotide; secretory protein; gene; ss.

Homo sapiens

WO200283876-A2

24-OCT-2002

27-MAR-2002; 2002WO-US09921

29-MAR-2001; 2001US-280067P.
29-MAR-2001; 2001US-291280P.
16-MAY-2001; 2001US-291280P.
17-MAY-2001; 2001US-291849P.
19-UN-2001; 2001US-2948P.
20-UN-2001; 2001US-2948P.

(INCY-) INCYTE GENOMICS INC

Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PB, Amshey SR;
CC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
J, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME; Dufour GE, Hillman JL, Daughtery SC, Dam TC, Peralta CH, David MH, Flores V, Marwaha R, à 

WPI; 2003-075543/07.

P-PSDB; ABP75660.

New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. AIDS), nor cancers - proliferations or cancers -

Claim 1; SEQ ID NO 267; 458pp + Sequence Listing; English.

The invention relates to a secretory polynucleotide (designated sptm)

comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a

naturally occurring polynucleotide sequence at least 90 % identical to

the polynucleotide sequence, a polynucleotide complementary to them or an

RNA equivalent of them. The polypeptide or polynucleotide are useful for

treating, preventing or diagnosing a disease or condition associated with

the expression of functional SPTM. These are particularly useful for

the expression of functional SPTM. These are particularly disorders

(e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's

disease), neurological disorders (e.g. epilepsy, Huntington's disease,

clasease), neurological disorders (e.g. epilepsy, Huntington's disease,

chementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,

chizophrenia or amresial, or cell proliferative disorders (e.g.

sochizophrenia or amresia), or cell proliferative disorders (e.g.

contacts of the brain,

leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,

leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,

cheast, cervix or prostate).

Note: The sequence data for this patent did not form part of the printed

syncopication, but was obtained in electronic format directly from WIPO at

comparisors.

Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 other;

99.28;

Query Match

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TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGTTCAGTGGGCCATGATCCCCGAGCTGC Gaps ; 0 Indels Score 1056; DB 25; Pred. No. 0; . ; 100.0%; Prec. ... Best Local Similarity .vv. Matches 1056; Conservative Local Similarity Н

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Length 1334;

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cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis, bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to medulate cellular adhesion. The reclular adhesion and/or medulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, medulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, and hematopoietic associated diseases and disorders, atelectasis, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, prochitis, pronchitis asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain hermiations, iatrogenic disease, inflammations, iatrogenic disease, inflammations, iatrogenic disease, inflammations, interaction of bone and viral meningitis, Alzheimer's Disease, cerebral
                                                                                                                                                            TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atlectash; pulmonary congestion; oedema: emphysema; chronic bronchitis; bronchial aschma; bronchiectash; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; holselmer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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                                                                                                                     cDNA clone encoding a human TANGO 261 polypeptide.
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AAA75163 standard; cDNA; 969
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hydrocephalus and encephalitis, and treat hepatic disorders.
note: the present sequence does not appear in the specification; it was
created using information provided.
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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer as well as for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                                                                                                          prostate tumour tissue; human; mammal; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identifying modulators of prostate cancer or agents that inhibit
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                                    ABK92120 standard; DNA; 1140 BP.
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08-DEC-2000; 2000US-0733288.

08-DEC-2000; 2000US-0733742.

24-JAN-2001; 2001US-27357F.

16-MAR-2001; 2001US-276791P.

16-MAR-2001; 2001US-276791P.

06-APR-2001; 2001US-281922P.

24-APR-2001; 2001US-286214P.

30-APR-2001; 2001US-286214P.

30-APR-2001; 2001US-286314P.
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Query Match Best Local Similarity 99.9 Matches 976; Conservative

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                                                                                                                                     cellular proliferation; cellular differentiation; cellular adhesion; von Milebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitels; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; acatiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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                                                                                                                    TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
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                                                             cDNA clone encoding a human TANGO 261 polypeptide.
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/product= "TANGO 261"
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                (first entry)
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P-PSDB; AAB18462.
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GCCGGGGGGCGCAACGCATCGTGGCCCTCCCCTCCCACCTCCCTGTGTATAATA 1000 125 340 400 220 280 185 245 460 580 305 520 GAGGAGCCCCCACCCTACCAGGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAG 485 640 545 700 605 760 665 820 725 880 785 940 965 GTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGG 6 ATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGATGATGGTG GAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGGCTCGGCCC CTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGAC CACAGCCAGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCG 246 Acceaccerdeccerdececerrececeradeceerrecacecerrecacece credalactealacedederecececacececealacadesecenterecacadesec GTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGG GAGAGCACAGTGTCAGGCAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCC GAGGAGCCCCCACCCTACCAGGGCCCCTGCACCTCCAGGGACCCCGAAGCAGCAG croarddaracraccaddcroddcccccccccccccccadaacrccodcarcadc GCCACGTGCTACGGCGCGCGGGCGCATGGAGGGGCCGCCGCCCCACCTACAGCGAGGTC ATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCCCCTCCTTG CTGGAGGGGACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGG CTGGAGGGGACCCGGCTCCACCACACACACACGCCCCCTAGAGAGGCGCAGCCATCTGG AGCAAAGAAAGGATAAACAGAAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCT GGGGCTGCGTAGGTGAAAAGGCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAGGAA CTGATGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGC GCCACGTGCTACGGCAGCGGGGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTC 1061 A 1061 161 99 821 941 221 126 281 186 341 306 366 486 546 401 461 521 426 581 641 . 107 909 761 999 881

RESULT 7 AAA75165

DB 21; Length 969;

Score 910; I Pred. No. 0;

85.8%; 99.9%;

Query Match Best Local Similarity

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WO200052022-A1 

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; halberiar disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                    TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                                                                             cDNA clone encoding a human TANGO 261 polypeptide.
     ВЪ
AAA75165 standard; cDNA; 969
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                               15-JAN-2001
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Homo sapiens

/\*tag= a /product= "TANGO 261" cocation/Qualifiers 6..764 /\*tag=

08-SEP-2000

01-MAR-2000; 2000WO-US05226

99US-0122458. 01-MAR-1999; (MILL-) MILLENNIUM PHARM INC

Holtzman DA, Barnes TM,

Fraser CC; Sharp JD, WPI; 2000-579269/54.

P-PSDB; AAB18463

Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -

Disclosure; Page -; 175pp; English.

describes TANGO 266, TANGO 261 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 262 cellular describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, arelectasis, cand hematopoietic associated diseases and disorders, spleen associated diseases and disorders, spleen associated as sense modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedems, hydrocephalus, brain herniations, iatrogenic disease, inflammations, and please, crebbral cerebral carbial and or all maningitis, Alzheimer's Disease, crebbral cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was created using information provided.

BP; 210 A; 317 C; 294 G; 148 T; 0 other; Sequence

ö 880 940 845 965 280 340 245 400 460 580 640 700 760 665 820 725 785 220 185 305 306 ACCTATCCGTACCTGCAGGAGGATCGACCTGCGGCCCACCATCTCGCTGTCAGACGGG 365 CTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACATCTTCGACAGTGAC 485 545 605 65 GTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGG acceacedeceres de consecuence de con ATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCCCCTCCTTG CTGGAGGGGACCCGGCTCCACCACACACACGCGCCCCTAGAGAGGGCAGCCATCTGG AGCAAAGAGAGATAAACAGAAAGGCACCCTCTCTAGGGTCCCCAGGGGGGCCGGGT GAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCC CTGATGGATAGTGCCAGGCTGGGCCGCCCTGCCCCCCCAGCAGAAACTCGGGCATAACTCAGC GCCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTC ATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTG CTGGAGGGGACCCGGCTCCACACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGG Argeceaacregagrirerreaarcarcarcarcargregregreargargargere GTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGG CACAGCCAGGGGGGGGGAGAGAAGATGCCCTGTCACAAGGATGCCTGTGGCCTTCG CACAGCCAGGGGGGGGAGAGAAGAAGATGCCCTGTCCTCAGACGGATGCCTGTGGCCTTCG ACCTATCCGTACCTGCAGCACGAGATCGACCTGCCCCCACCATCTCGCTGTCAGACGGG GAGGAGCCCCCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAG AGCAAAGAAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGCCCGGGCT GGGGCTGCGTAGGTGAAAAGGCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAAAAA ATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGATGGTGATGGTG ACCGACCGCCTGGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCC Gaps ö Length 969; 1; Indels DB 21; 0; Mismatches ö Score 910; Pred. No. 85.8%; Matches 960; Conservative Best Local Similarity A 1061 996 4 1061 ø 161 99 221 126 281 186 341 246 401 366 426 486 641 701 909 999 821 726 786 846 1001 906 461 521 581 546 761 881 941 996 Query Match ò 엄 ò 셤 ઠે g ઠે 요 ò 요 à 원 ઠ g ò 유 ò 셤 ò 셤 ò 셤 ò 셤 δ 셤 ò 셤 ò 셤 ð g ò

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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as all coalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Sydrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin'inhibin activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hamemostatic; amyotrophic lateral sclerosis; SNy Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, W. Zhang J;
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Yang Y,
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Pred. No. 0;
0; Mismatches
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO 71.
                                                          AAI57868 standard; cDNA; 1066
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25-ARR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-OCT-2000; 2000US-0653450.
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TTGTTCAGATCATCATCATCGTGGTGGTGATGGTGGTGGTGGTGGTCACGTGCC
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The invention relates to an isolated nucleic acid molecule encoding a Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences A1761441.1, A1594390, M 004338 and A217461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IER-1, VDUP-1, BTG-2 and TIS-11d or its comprising MIVR-1, televanishing if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and lisorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, streating-cell-death of cardiac hypertrophy, myocardial infarction, streating-cell-cells and heart failure. The present sequence
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                                                                                                                                                                                                                           /product= "MIVR-1"
/note= "This region is specifically claimed in claim 3"
               Human, 88; gene, MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
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Pred. No. 1.5e-289;
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                                                                                                                                                                        Location/Qualifiers
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P-PSDB; AAU78231.
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
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Prostate specific nucleic acid DEX0259 32. AAGAGACTTGCAAAAAAAAAA 1058 Claim 1; Page 166-167; 242pp; English ΰ Liu BP. ABS61424 standard; cDNA; 1583 ŝ 01-NOV-2001; 2001WO-US45654. 01-NOV-2000; 2000US-244782P 05-NOV-2002 (first entry) Chen (DIAD-) DIADEXUS INC WPI; 2002-490217/52. Recipon H, WO200242776-A2. Homo sapiens 30-MAY-2002 algorithms 1035 384 264 915 144 84 24 ABS61424; 444 735 324 855 204 975 919 919 795 Sun Y, RESULT 11 ABS61424 염 유 ò g ò 임 ò g ò 셤 ò g ò g ò ò .; The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, mimunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as immune system suppression, Activin/inhibin activity, chemotactis/chemokinetic activity, heametactis/and therapy, drug screening, and thrombolytic activity, arthritis and inflammation, leukaemias and 195 445 865 255 802 315 745 375 685 435 625 495 565 555 505 615 C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification. ü, CGTGGTGGTGATGATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCT CTCAGAAGGATGCCTGTGGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCC GCCCACTATTTCGCTGTCGGACGGGGAGGACCCCCACCTACCAGGGCCCCTGCACC CTCAGAAGGATGCCTGTGGCCCTCGGAGGCACAGTGTCAGGCAACGGAATCCCAGAGCC GCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCG GGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGGACGAGATCGACCTGCC GGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCC GCCCACCATCTCGCTGTCAGACGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCT CCAGCTTCGGGACCCCGAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCC AAACAGAACCATCTTCGACAGTGACCTGGATAGTGCCAGGCTGGGCGGCCCCTGCCC Gaps Wang l nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries -1; . ز Ren F, Zhang J Length 1069; Indels Qian XB, Yang Y, Sequence 1069 BP; 176 A; 323 C; 346 G; 222 T; 2 other; Score 548; DB 22; Pred. No. 2.8e-209; 0; Mismatches 5; Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT; Claim 1; SEQ ID NO 3643; 10078pp; English. Asundi V, Cher Wehrman T, Xu , Goodrich R, I 2000US-0653450. 2000US-0662191. 2000US-0693036. 2000US-0727344. Query Match
Best Local Similarity 99.4%;
Matches 918; Conservative WPI; 2001-442253/47. P-PSDB; AAM40498. Liu C, F Wang Z, V Zhou P, (HYSE-) HYSEQ INC 03-AUG-2000; 2 14-SEP-2000; 2 19-OCT-2000; 2 29-NOV-2000; é ΥΤ, J, 136 196 864 256 804 316 744 376 684 436 624 496 564 556 504 Novel Tang Wang Zhao anch

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CCCTCCCACCTCCCTGTGTATAAATATTTACATGTGATGTCTGGTCTGAATGCACAAGCT 1034 202 675 734 325 794 265 854 914 145 GCTTCTTAGAAGAGGAGTGAGAAGGCGGGGGGGCGCAGCAACGCATCGTGTGGCCCTC 974 82 25 The invention relates to an isolated polypeptide comprising a sequence with 60 % identity to one of prostate specific protein (PSP) sequences, GCCGCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACC CGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGGAGAAAGGATAAACAGAAAGGACACCCTC TCTAGGGTCCCCAGGGGGCCGGGCTGGGGGCTGCGTAGGTGAAAAGGCAGAACACTCCGC GCTTCTTATAAGAGGAGTGAGAGAAGGCGGGGGCGCCAGCAACGCATCGTGTGGCCTC ccccascastractroscerareaceccacerectroscerascesceses CGCCCCTAGAGAGCGCCAGCCATCTGGAGCAAAGAAGGATAAACAGGAAAGGACACCCTC TCTAGGGTCCCCCAGGGGGGCCGGGCTGCGCTGAGGTGAAAAGGCAGAACACTCCGC CCCTCCCACCTCCCTGTATAAATAATTACATGTGATGTCTGGTCTGAATGCACAAGCT and GCCGCCG-CCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTTCCAGCACC New polypeptide useful for diagnosing and monitoring the presence metastases of prostate cancer in a patient and as a component in databases for search analysis as well as in sequence analysis Human; se; prostate specific nucleic acid; PSNA; prostate cancer; cytostatic; non-cancerous prostate disease; PSP; vaccine; prostate specific protein; metastasis.

relevant gene; toxicological response; gene; ss.

Toxicologically

WO2003016500-A2. Homo sapiens.

16-AUG-2002; 2002WO-US26514. 16-AUG-2001; 2001US-313080P.

Toxicologically relevant human nucleotide sequence

14-MAY-2003 (first entry)

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prostate specific nucleic acids sequences, PSNA, (or a sequence that hybridises to it or is 60% identical to it), given in the specification. Also included are a vector comprising the polynucleotide, a host cell comprising the vector, an antibody specific for the PSP proteins and a vaccine comprising the protein or polynucleotide. The PSP and PSNA are useful for diagnosing and annitoring the presence and metastases of prostate cancer in a patient. The PSNA is useful for the level PSNA in a sample. An antibody to the PSP is useful for determining the presence of prostate specific protein in a sample, and for treating a patient with prostate cancer, which induces an immune response against the prostate cancer cell expressing the nucleic acid or polypeptide and a kit is useful for detecting a risk of cancer or presence of cancer in a patient. PSNA is useful as hybridisation probes to detect, characterise and quantify hybridising nucleic acids from both genomic and transcript-derived nucleic acid samples and also in databases for search analysis as well as in sequence analysis algorithms. PSNA is useful to drive in vivo expression of PSP. The present
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Sequence 1583 BP; 361 A; 469 C; 457 G; 296 T; 0 other;

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                                                                                                              373 GCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCT
                                                                                                                                     887 GCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCT
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48.0%; Score 509; DB 24; Length 1583; 99.8%; Pred. No. 9.9e-194;
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The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genee to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynuclecides selected corner to expension of the partial sequences given in AB282842 to ABZ84764, or their fragments of at least 20 nucleotides or homologues; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a muman subject to a known toxic pharmaceutical or industrial agent, comprising: (a) expossing cells to an agent or isolating the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or comparing the tes
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                                                                                                                                                                                                                                                                                                                                  Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity -
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                                                                                              Pickett GG,
(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
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ABZ84732 standard; cDNA; 474 BP.

ABZ84732, 8XH

ABZ84733

Sequence 408 BP; 81 A; 159 C; 115 G; 53 T; 0 other;

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The present sequence is one of 3351 sequences in a library of human polymucleotides. The library is used to detect differentially expressed genes cortelated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polymucleotides. The probes can be used for chromosome mapping of the polymucleotides. The probes can be used for chromosome mapping of the polymucleotides and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polymucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and produces at the polymucleotides, polymeptides and produces against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, cypplasia and hyperplasia.
                                                                                                                              959
 536
                                                                 296
                                                                               Innis MA, Garcia PD, Klinger J, Kassam A, Kennedy GC, Pot D, Lamson G, Drmanac R; Dickson M, Labat I, Leshkowitiz D; LW, Strache-Crain B;
                              GGCTGGGCGGCCCCTGCCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCA
                                                                                                                                                                                             GCGGCGGCGCATGGAGGGCCGCCCCACCTACAGCGAGGTCATCGGCCACTA 711
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or
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytostatic; gene therapy; colon cancer; prostate cancer;
breast cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polynucleotide, SEQ ID NO: 1739
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                                                                                                                                                                                                                                                                                                           AAF65983 standard; cDNA; 408 BP
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Crkenjakov R, Drmanac S,
Kita D, Garcia V, Jones
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Reinhard C,
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical
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                                                                          8 GATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAG
                                                                                                                                  68 CCAGGGGGGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGGGAGAG
                                                                                                                                                                                                                                                 188 CCGCCTGGCCGTCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTA
                                                        166 GATCACGTGCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAG
                                                                                                                 CCAGGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAG
                                                                                                                                                                      CACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGGCCTCGGCCCACCGA
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                             Gaps
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Length 408;
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                            1; Indels
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Score 350; DB 22;
Pred. No. 3.5e-130;
0; Mismatches 1;
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 33.0%;
99.8%;
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              Best Local Similarity 99.8
Matches 400; Conservative
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compositions for treatment of pancreatic tumors. AAS52858-253014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented
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                                                                                                                                                                                                                                                                             Gaps
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Receptor-1 polypeptide, useful for treating cardiovascular diseases
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                                                                                                                                                                                                         Query Match 30.3%; Score 322; DB 20; Length 812; Best Local Similarity 100.0%; Pred. No. 5e-119; Matches 322; Conservative 0; Mismatches 0; Indels .
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                                                                                                                                                 Sequence 812 BP; 157 A; 272 C; 237 G; 146 T; 0 other;
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The invention relates to an isolated nucleic acid molecule encoding a Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences AIY6141.1, A1594390, MM 004338 and AQ177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of they are molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising wilth. Totating a molecule having cardiac cell anti-apoptotic activity is expression product, determining if the anti-apoptotic activity is computated and thereby identifying a modulator. The cardiac cell anti-treating, diagnosing and monitoring progression of such diseases and disorders as characterised by increased apoptotic cell-death of vascular cellsers as characterised by increased apoptotic cell-death of vascular cellsers as characterised by increased apoptotic cell-death of vascular cellsers as characterised by increased apoptotic cell-death of vascular cellsers as characterised by increased apoptotic cell-death of vascular cellsers as characterised by increased apoptotic cell-death of vascular cellsers as characterised by increased apoptotic cell-death of vascular cells e.g. cardiac hypertrophy, mycardial infarction, stroke, arteriosclerosis and heart failure. The present sequence is one of the four Genbank sequences (AI761411.1) which are homologous to the cDNA for human MIVR-1 and which are specifically disclaimed.
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Pred. No. 2e-115;
0; Mismatches 3; Indels 1
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99.3%;
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Best Local Similarity 99.3
Matches 583; Conservative
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Search completed: December 8, 2003, 04:24:34 Job time : 348 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.		December 8, 2003, 03:57:35 ; Search time 80 Seconds (without alignments)
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Copyright	OM nucleic - nucleic search, using sw model	December 8,
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Title: Perfect score: Sequence:

569978 seqs, 220691566 residues OLIGO\_NUC Gapop\_60.0 , Gapext 60.0 Scoring table: Searched:

Word size :

1139956 Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

198ued Patents NA:\*
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	912	86.0	1140	4	US-09-769-482-1	Sequence 1, Appli
~	708	66.7	759	4	US-09-769-482-2	'n
e	24	2.3	24	4	US-09-769-482-5	'n
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r O	24	2.3	24	4	US-09-769-482-10	70,
9	23	2.5	377	~	US-08-332-766A-1	Sequence 1, Appli
7	21	2.0	22	4	US-09-769-482-7	7
80	21	2.0	989	7	US-08-522-421-7	7,
O	21	2.0	1327	-	US-08-165-315D-3	m
C 10	21	2.0	8252	Н	US-08-046-585-15	Sequence 15, Appl
c 11	21	2.0	8252	ч	US-08-393-703-15	15
c 15	21	2.0	8252	'n	PCT-US93-11721-15	15
c 13	21	2.0	1664976	4	US-08-916-421B-1	1
14	20	1.9	20	4	US-09-769-482-9	Sequence 9, Appli
c 15	20	1.9	20	٣	US-08-753-247-22	22
16	20	1.9	51	m	US-08-753-247-23	23
17	20	1.9	588	٣	US-08-744-138-1	Ļ
18	20	1.9	588	4	US-09-241-376-1	H
19	20	1.9	1189	7	US-07-781-034-4	4,
20	20	1.9	1189	'n	PCT-US92-08328-4	4
21	20	1.9	1218	4	US-09-685-853A-1	Ļ,
22	20	1.9	1479	-	US-08-249-112-2	7
23	20	1.9	1479	Ŋ	PCT-US95-06556-2	7
24	20	1.9	1531	~	US-08-948-176-24	Sequence 24, Appl
25	20	1.9	2887	m		'n
56	20	1.9	319608	4	-09-539-3	٦,
27	20	1.9	319608	4	US-09-679-409-1	7,

Sequence 9, Appli Sequence 10, Appl Sequence 27, Appl Sequence 28, Appl	Sequence 27, Appl Sequence 28, Appl Sequence 69, Appl	Sequence 11, Appl Sequence 12, Appl Sequence 36, Appl	Sequence 36, Appl Sequence 129, App Sequence 130, App Sequence 30, Appl	Sequence 139, App Sequence 1, Appli Sequence 116, App Sequence 3, Appli
US-09-438-268-9 US-09-438-268-10 US-08-155-171B-27 US-08-155-171B-28	US-08-435-998-27 US-08-435-998-28 US-09-813-781-69	US-09-438-268-11 US-09-438-268-12 US-08-155-171B-36	US-08-435-998-36 US-08-142-551B-129 US-08-142-551B-130 US-08-332-766A-30	US-09-385-982-139 US-08-329-055-1 US-08-998-416-116 US-08-865-297-3
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### ALIGNMENTS

TYPE: DNA CRGNNISM: Homo sapiens FRATURE: MAMM/KEY: CDS COCATION: (95)(850)	
Query Match         86.0%;         Score 912;         DB 4;         Length 1140;           Best Local Similarity         99.9%;         Pred. No. 0;         1;         Indels         0;         Gaps           Matches         962;         Conservative         0;         Mismatches         1;         Indels         0;         Gaps           95         CAGGCAATGGCGAGTTTGTTCAGATCATCATCATCATGTGGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGT	e 912; DB 4; Length 1140; . No. 0; ismatches 1; Indels 0; Gaps 0; GTTCAGATCATCATCATGATGATGATGATGATGATGATGATCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGA

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Sequence 2. Application US/09769482

Sequence 2. Application US/09769482

Sequence 2. Application US/09769482

GENERAL INFORMATION:

APPLICANT: SRIVANION WILL

APPLICANT: WULL JUDD W.

APPLICANT: STORMA, TAKEHIKO

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

FILE REFERENCE: 04995.0657-0000

CURRENT PILING DATE: 2001-01-26

FRICR PAPLICATION NUMBER: 60/178,772

FRICR PAPLICATION NUMBER: 60/178,772

FRICR FILING DATE: 2000-01-28

FRICR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 67

SOFTWARRE: PATCHIN VET. 2.1

SEQ ID NO 2
509 CAGCAGCTGGAACTGAACCGGGGGTGGTCGCGCACCCCCAAACAGAACCATCTTCGAC
                                                                                                                                                                                              AGTGACCTGATGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGC
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GTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGG
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                                                                                                                                                Gaps
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US-09-769-482-5
US-09-769-656130
; Sequence 5, Application US/09769482
; Sequence 5, Application US/09769482
; Retent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSYNICLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
                                                                                                                                                ;
0
                                                                                                       Length 759
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAG 859
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                                                                                                       Score 708; DB 4;
Pred. No. 1e-271;
                                                                                                                                                0; Mismatches
                                                                                                     66.7%;
                                                                                                                                                Matches 758; Conservative
LENGTH: 759
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                          Similarity
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                                                                                                       Query Match
Best Local
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360

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460

420 580 480 640 540 700 600 660 820 720

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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-769-482-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version WRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08332766A
Patent No. 5843647
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: ARMOUR, John
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE DERESS:
ADDRESSEE: CUSHWAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR PILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 10
LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.3%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.2%; Score 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAWE: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 GAATGCACAAGCTAAGAGAGCTTG 1
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 377 base pairs
nucleic acid
EDNESS: single
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LENGTH: 377 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: SRIVASTAVA, SHIV
| APPLICANT: MOUL, JUDD W.
| APPLICANT: MOUL, JUDD W.
| APPLICANT: MOUL, JUDD W.
| APPLICANT: MOUL, JUDD W.
| APPLICANT: SEGAWA, TAKEHIKO
| TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
| FILE REFERENCE: 04995.0057-00000
| CURRENT APPLICATION NUMBER: US/09/769,482
| CURRENT APPLICATION NUMBER: 60/178,772
| PRIOR PILING DATE: 2000-01-28
| PRIOR PILING DATE: 2000-01-31
| NUMBER OF SEQ ID NOS: 67
| SOFTWARE: PALENTIN VET: 2.1
| SEQ ID NO 6
| LENGTH: 24
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TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-769-482-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.3%; Score 24; DB 4; Length 24; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 0; Indels
                             FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT APPLICATION NUMBER: 05.01-01-26
FRIOR APPLICATION NUMBER: 60/179,72
PRIOR FILING DATE: 2000-01-28
FRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1022 GAATGCACAAGCTAAGAGATTG 1045
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Sequence 10, Application US/09769482
Patent No. 6566130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09769482 Patent No. 6566130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                  Sequence 7. Application US/09769482
| Sequence 7. Application US/09769482
| Patent No. 6566130
| GENERAL INFORMATION:
| APPLICANT: SRIVASTANA, SHIV
| APPLICANT: MOUL, JUDD W. |
| APPLICANT: WU, LINDA L. |
| APPLICANT: SEGAWA, TAKEHIKO |
| TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED |
| TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED |
| TITLE OF INVENTION: PROSTATE SOURCE |
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY |
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY |
| TITLE OF INVENTION NUMBER: US/09/769, 482 |
| FILE REFERENCE: 04995.0057-00000 |
| CURRENT APPLICATION NUMBER: 60/179, 045 |
| PRIOR FILING DATE: 2000-01-31 |
| NUMBER OF SEQ ID NOS: 67 |
| SEGTWARE: PALEATIN VET. 2.1 |
| SEG IN NO. 7 |
| SEGTWARE: PALEATIN VET. 2.1
                         Gaps
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APPLICANT: Abu-Bakar, Umi Kalsom
APPLICANT: Gallego-Veigas, Pedro Pablo
APPLICANT: Gallego-Veigas, Pedro Pablo
APPLICANT: Gray, Julie Elizabeth
APPLICANT: Grierson, Donald
APPLICANT: Picton, Steve
APPLICANT: Picton, Steve
APPLICANT: Picton, Steve
APPLICANT: Picton, Dave of Davidson
APPLICANT: Picton, Lee Colin
TITLE OF INVENTION: DRA, DAA CONSTRUCTS, CELLS AND PLANTS
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillah...
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-769-482-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 22;
22;
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                         Indels
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  Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 22; Matches 21; Conservative 0; Mismatches
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 23; Conservative 0; Mismatches
                                                                        138 TGGTGGTGATGATGGTGTG 160
                                                                                                                     123 redredredredredredredre 145
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CTTGGGTTCGGGTGAAAGCGC 26
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ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                    US-09-769-482-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-522-421-7
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LENGTH: 22
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.0%; Score 21; DB 2;
00.0%; Pred. No. 15;
APPLICATION NUMBER: US/08/522,421
CLASSIPICATION NUMBER: US/08/522,421
FILING DATE: 11-JAN-1996
CLASSIPICATION DATA:
APPLICATION NUMBER: GB 9305868.3
FILING DATE: 22-MAR-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9305869.1
FILING DATE: 22-MAR-1993
FRICH APPLICATION NUMBER: GB 9305865.9
FILING DATE: 22-MAR-1993
FRICH APPLICATION NUMBER: GB 9305865.9
FILING DATE: 22-MAR-1993
FRICH APPLICATION NUMBER: GB 9305865.7
FRICH APPLICATION NUMBER: GB 9305865.7
FRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9305867.5
FILING DATE: 22-MAR-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9305867.5
FILING DATE: 22-MAR-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9305862.6
FILING DATE: 22-MAR-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9305862.6
FILING DATE: 22-MAR-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9314351.9
FRICH DATE: 12-JUL-1993
FRICH DATE: 12-JUL-1993
FRICH DATE: 12-OCCT-1993
FRICH DATE: 12-OCCT-1993
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08165315D
Patent No. 5525716
GENERAL INFORMATION:
APPLICANT: Odd-Arne Olsen
APPLICANT: Roger Kalla
TITLE OF INVENTION: Promoter
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge, Steward, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1041 GCTTGCAAAAAAAAAAAA 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 GCTTGCAAAAAAAAAAAAA 683
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100.0%; Pre-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 686 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.0
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Connecticut
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDN/
ORIGINAL SOURCE:
ORGANISM: ERT17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 06905
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INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 8252 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-393-703-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US93-11721-15/c
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US-08-393-703-15/c
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| Sequence 15, Application US/08046585 |
| Patent No. 5453362 |
| Patent No. 5453362 |
| Patent No. 5453362 |
| Patent No. 545362 |
| Patent No. 545362 |
| APPLICANT: Lamarco, Kelly |
| APPLICANT: Wilson, Angus |
| APPLICANT: Herr, Winship |
| TITLE OF INVENTION: HOST CELL FACTOR |
| NUMBER OF SEQUENCES: 15 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT |
| STREET: 4 Embarcadero Center, Suite 3400 |
| STATE: CA |
| COUNTRY: USA |
| COUNT
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 14; Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      NAME: MATY M. Krineky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 2105-P0001
TELECHONE: 201-324-6155
TELEPHONE: 201-324-6156
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,315D
FILING DATE: 10 December 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324707.0
FILING DATE: 2 December 1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAI, RICHARA A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: Ltp2 gene
US-08-165-315D-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: DNA
FRAGMENT TYPE: gene
FEATURE:
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TELEX: 91
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APPLICANT: Wilson, Angus
APPLICANT: Wilson, Angus
APPLICANT: Wilson, Angus
APPLICANT: Wilson, Angus
APPLICANT: Wilson,
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
NUMBER OF SEQUENCE: 15
CORRESPONDENCE: 15
CORRESPONDENCE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 8 EMBERT
GITY: San Francisco
Query Match 2.0%; Score 21; DB 1; Length 8252; Best Local Similarity 100.0%; Pred. No. 11; Matches 21; Conservative 0; Mismatches 0; Indels
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Pred. No. 11;
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ZIP: 94111-4187

COUNTEX READABLE FORM:

MEDIUW TYEE: FIDEPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,703

FILING DATE: 24-FRE-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: A-57503-2/RAO

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION INFORMATION:

TELECOMMUNICATI
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Mismatches
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                                                                                                                                                                                                                  138 TGGTGGTGATGATGGTGATGG 158
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, Patent No. 5585239
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Best Local Similarity 100.0%; Pi
Matches 21; Conservative 0;
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LOCATION: (559167). (559167)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEX: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (231980)...(231980)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234187)...(234187)
OTHER INFORMATION: n equals a, t
                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCATION: (191989)...(191989)

THER INFORMATION: n equals a,
AMB/KEY: misc. feature
COCATION: (191995)...(19195)

THER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (312837)...(312837)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                      ION: (84812)..(84812)
INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                            AAME/KEY: misc feature
LOCATION: (98239) .. (98239)
THER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (234814) .. (234814)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
COCATION: (103998)..(103998)
THER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (163385). (163385)
DTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (234220) . (234220)
OTHER INFORMATION: n equals a,
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                                                                                                                                                                                                                                                                                                       JOCATION: (98120)..(98120)
THER INFORMATION: n equals a,
      n equals a,
                                                                                     NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals
                      YEY: misc feature
TION: (28257)..(28258)
IINFORMATION: n equals
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                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (84812)..(84
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Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
FILE REFERENCE: 1997-08-22
RIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
RIOR REPLIANG DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                          APPLICANT: Lamarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL PACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 8252;
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                                                                                                                                                 NUMBER OF SEQUENCES: 15
CORRESPONDENCE PUBLES: 15
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11721

FILING DATE: 03-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gomean Richard A REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 36,627

REFERENCE/DOCKET NUMBER: FP-57503-1/RAO

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 791-1989

TELEFAX: (415) 791-1989

TELEFX: 910 277299

TELEFX: 910 277299

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 11; Matches 21; Conservative 0; Mismatches
equence 15, Application PC/TUS9311721 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2748 TGCTGCTGATGATGGTGATGG 2728
                                                                                                                                                                                                                                                                                                 ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TGGTGGTGATGATGGTGATGG 158
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ORGANISM: Methanococcus jannaschii
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NAME/KEY: misc feature
LOCATION: (28222)..(28222)
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TYPE: nucleic acid
STRANDEDNESS: double
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PCT-US93-11721-15
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NAME/KEY: misc feature
LOCATION: (60092)..(60092)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (657081)..(657081)

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OTHER INFORMATION: n equals a,

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NAME/KEY: misc feature duding a, v. CATION: (65723). (65723) (65723) (65723) (65723) (65723) (65723) (65723) (65723) (65723) (677435) (677435) (677435) (677435) (677435) (677435) (677435) (677435) (77748; misc feature LOCATION: (68242) (68242) (7778; misc feature LOCATION: (71362) (71362) (77362) (77362) (77362)

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NAME/KEY: misc feature
LOCATION: (741684)...(741684)
LOCATION: (741684)...(741684)
NAME/KEY: misc feature
LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (779676)...(779676)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (85539)...(855539)
OTHER INFORMATION: n equals a, t,
LOCATION: (85539)...(855539)
OTHER INFORMATION: n equals a, t,
LOCATION: (87676)...(871619)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (87676)...(871619)
OTHER INFORMATION: n equals a, t,

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NAME/KEY: misc\_feature LOCATION: (1084830) .(1084830) OTHER INFORMATION: n equals a,

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NAME/KEY: misc\_feature LOCATION: (1096646)...(1096846) OTHER INPORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1119881)...(1119881) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1130681)...(1130881) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1310988)...(1310988) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1310988)...(1310988) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1313224)...(131224)

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LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a,

NAME/KEY: misc feature LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a,

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NAME/KEY: misc feature LOCATION: (1349491)..(1349491) OTHER INFORMATION: n equals a,

NAME/KEY: misc feature LOCATION: (1470091)..(1470091) OTHER INFORMATION: n equals a,

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LOCATION: (1569020)..(1569020) OTHER INFORMATION: n equals a,

NAME/KEY: misc\_feature

INFORMATION: n equals a, t, c, or

WAME/KEY: misc\_feature

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APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Falko-Guenther
APPLICANT: DORNER, Filed-cich
APPLICANT: DORNER, Friedrich
APPLICANT: EIBL, Johann
TITLE OF INVENTION: DERLVATIVE OR A DERLVATIVE OF A FURIN
TITLE OF INVENTION: HTTEROLOGOUS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT APPLICATION NUMBER: 00/178,72
PRIOR FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VOR: 2.1
SOFTWARE: PATENTIN VOR: 2.1
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; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-769-482-9
                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 5.,
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138 TGGTGGTGATGATGGTGATGG 158
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Patent No. 6210929
GENERAL INFORMATION:
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Patent No. 6566130
                                                                                                                                                                                    Query Match
2.0%; Sci
Best Local Similarity 100.0%; P.
Matches 21; Conservative 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
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CORRESPONDENCE ADDRESS:
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CITY: Washington

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1.9%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels
CITY: Washingcom.
STATE: D.C.
COUNTRY: USA
COUNTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 22-NOV-1996
CLASSIFICATION NUMBER: US/08/753,247
FILING DATE: 24-NOV-1996
CLASSIFICATION NUMBER: US/08/753,247
FILING DATE: 24-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 20,768
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPHONE: GLOS/672-5300
TELEPHONE: GLOS
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Search completed: December 8, 2003, 06:19:08 Job time: 85 secs

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                                                                                                                                                       December 8, 2003, 03:56:15 ; Search time 2638 Seconds (without alignments) 9775.227 Million cell updates/sec
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                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45562784
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22781392 seqs, 12152238056 residues
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                                                                                                     OM nucleic - nucleic search, using sw model
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13 BQ641849
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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### ALIGNMENTS

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Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:6292265"
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                                                                                                                                                                /clone="UI-H-EZ1-bbg-h-14-0-UI"
/tissue type="Chondrosarcoma Grade II"
/dvy stage="Adult"
/lab_host="DH108 (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 68.0%; Score 722; DB 13; L 11 Similarity 100.0%; Pred. No. 1.3e-150; 722; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=grade-2-chondrosarcoma
                                                                                 organism="Homo sapiens"
                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_SEQ=ATCTAATATG"
_213 c 253 q
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TAG_LIB=UI-H-EZ1
TAG_TISSUE=grade
POLYA=Yes.
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/tissue_trape_normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
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/lab_host="DH10B (phage-resistant)"
/lone_lib="MIH MGG-47"
/lone="Organ: eys Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library. |"
Note: this is a NIH MGC Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              967 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8287174 NIH_MGC_43 Homo saplens cDNA clone IMAGE:6292265
5', mRNA Sequence.
                                                                                                                                                                                                     107 GAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGGTGGTG 166
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 967)

                                                                                                                                                                                                                                         69 AAATATTTACATGTGTGTCTGGTCTGAATGCACAAGCTAAGAGAGCTTGCAAAAAAA 10
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Tissue Procurement: ATC
CNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2493 row: g column: 18
High quality sequence stop: 571.
Location/Qualifiers
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                                                                   936 AGGAAGGCGGGGGGCGCAGCAACGCATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTAT
                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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99.9%; Pred. No. 3.8e-138;
live 0; Mismatches 1;
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Query Match
Best Local Similarity 100.
Matches 652; Conservative
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1 (bases 1 to 655).
11H-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
          ACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGAC
                                                                                                                            CCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGGAG
                                                                                                                                          CCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAA
                                                                                                CCCCCACCTACCAGGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGGAA
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                                         ACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGGCCTCGGCCCCACCGAC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2367 row: g column: 20
High quality sequence stop: 645.
                                                                                                                                                                                                                                                                                                                                                                                          GGGACCCGGCTCCACACACACACACACGCGCCCCTAGAGAGCGCAGCCATCTGGAG
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ691705.1 GI:21817021
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Homo sapiens
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/clone="IMAGE:6208939"
/tissue_type="ductal carcinoma, cell line"
/lab_host="NHAGE:0208939"
/tissue_type="ductal carcinoma, cell line"
/lab_host="NHIOB (phage-resistant)"
/clone lib="NHH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the
following 5' adaptor: GGGAGGGG, Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                   Length
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100.0%; Pred. No. 4e-135;
iive 0; Mismatches 0;
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BQ6367
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 951)

Li,W B., Gruber,C., Jessee,J. and Polayes,D.
Full.length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12903836.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRX cedex - France

Email: seqref@genoscope.cns.fr, www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

9945.r. For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODJ015DC06NP1&cluster=9945.r. Contact :
Feng Liang Email: filangelifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODJ015DC06NP1.
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/mol_type="mRNA"
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llarity 99.6%; Pred. No. 2.9e-135;
Conservative 0; Mismatches 3;
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Wistow,G., Bernetein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
Mol. vis. 8 (4), (2002) In press
Contact: Wistow G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ636742 609 bp mRNA linear EST 15-JUL-2002 hd13h06.yl Human Retina cDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone hd13h06 5', mRNA sequence.
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/dev stage="Adult"
/dab_host="EMDH108"
/clone_lib="Human Retina cDNA (Un-normalized, unamplified
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 609)
                              ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGGAGG
                                                                                                                                              GGACCCGGCTCCACCACACACACACACACCCCTAGAGAGCGCAGCATCTGGAGCAAAG
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National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6/31, NIH, Betheeda, MD 20892-2740, USA Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 13 row: h column: 06
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="hd13h06"
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AGENCOURT_8046394 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209341
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Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTACTTCTACATCGTAGCGGCGCCGCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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1 (bases 1 to 890)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                  TCGGCCCACCGACCGCCTGGCCGTGCCCCTTCGCCCAGCGGGGGGGCGTTCCACGCTT
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                                                                                                  Length 609;
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TITLE
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/organism="Homo sapiens"

/mol_type="mRNA"

/do_tref="mRNA"

/do_tref="warson:9606"

/clone="IMAGE:620941"

/tissue_type="ductal carcinoma, cell line"

/tissue_type="ductal carcinoma, cell line"

/lab host="DH108 (phage-resistant)"

/clone=lib="MIH_MGC_110"

/clone=lib="MIH_MGC_110"

/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRIX/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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                                                           CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MG clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2368 row: h column: 14
High quality sequence stop: 627.
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  Ph.D.
Contact: Robert Strausberg, E
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 99.8
Matches 651; Conservative
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                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.inih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
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1 (bases 1 to 602)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Umpublished
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564 GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 GGAGCCCCCACCCTACCAGGGCCCCTGCACCTTCCAGCTTCGGGACCCCCGAGCAGCAGCTT
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                                       624 GGCGGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTAC 675
                         601 GGGCGGCCCCCCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGTGCTAC 652
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                                                                                                                                                                                                                                                                                                                                                                                                        from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
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_179 c 196 g
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                                                                                                                                                                     CA431191.1 GI:24793917
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Homo sapiens
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DEFINITION
                                                                                         RESULT 7
CA431191/c
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ORIGIN
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Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
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483
                                                               642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 588)
NGT-GARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                               362 CGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCCCCCCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 GGAGGGACCCGGCTCCACCACACACACACACCCCTAGAGAGGGCGCAGCCATCTGGAG
                                                                                                                            482 GATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGC
                                                                                                                                                                                         CACGTGCTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCAT
   542 GGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FGI-bgi-f-22-0-UI"
/tissuc_type="Rcll lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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GI:23654753

BU730650.1

4.oligo.rst

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/clone lib="NCI CGAP FGI"
/note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP FGI is a normalized cDNA library obtained from a pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGTCACTC. The cell lines were provided by Dr. James Martin from the University of lowa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 ACCAGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGG
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                                                                                                                                                                                                                                                                                                                                    TAG_LIB=UI-H-FGI
TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_SEQ=CGGTCGTC"
176 c 188 g 142 t
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100.0%; Pred. No. 2...
0; Mismatches
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Matches 585; (
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BU730650 629 bp mRNA linear EST 09-OCT-2002 UI-B-CII-afq-o-09-0-UI.81 UI-B-CII Homo sapiens cDNA clone UI-B-CII-afq-o-09-0-UI 3', mRNA sequence.

LOCUS DEFINITION BU730650/c

RESULT 9

ACCESSION

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/dev_stage="RPE and Choroid"
/dev_stage="DH108 [Life Technologies] (Tl phage resistant)"
/clone_lib="UI-E-CII"
/clone_lib="UI-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coordinated Laboratory
Coordinated Laboratory
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Bmail: bentco-soares@ulowa.edu
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
Location/Qualifiers
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/mol type="mRNA"
/db_xrep="type="mRNA"
/clone="INAGE:336369"
/tissue_type="glioblastoma (pooled)"
/lab_bost="mR10"
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/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological blasorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
Ph.D.
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                                                                                                                                                                                Score 559; DB 10; L
Pred. No. 1.5e-114;
0; Mismatches 0;
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Genome Res: 6 (9), 791-806 (1996)
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100.0%; Pre
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Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Gualifiers

| Organism="Homo sapiens" |
| Abb_xxef="taxon:9606" |
| CiDne="UD-"EXL-bbf-f-09-0-UI" |
| Abb_host="DH-BEXL-bbf-f-09-0-UI" |
| Abb_host="DH10B (Life Technologies)" |
| CiDne=lib="UCGAP_CAP" |
| Abb_host="DH10B (Life Technologies)" |
| CiDne lib="CAP CAP" |
| Abb_host="DH10B (Life Technologies)" |
| Abb_host="DH10B (Life Technologies)" |
| CiDne lib="Sister (SPR I) |
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Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthoapedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
DOLYA-YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ575582 570 bp mRNA linear EST 19-JUN-2002 UI-H-EZ1-bbf-f-09-0-UI.sl NCI CGAP_Ch2 Homo sapiens cDNA clone UI-H-EZ1-bbf-f-09-0-UI 3', mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 570)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 CCCTGTGTATAAATATTTACATGTGATGTCTGGTCTGAATGCACAAGCTAAGAGAGCTTG
                                                                                              259 AGGGCAGCCATCTGGAGCAAAGGAAAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGTGTATAAATATTTACATGTGTGTGTGTGTGAAATGCACAAGCTAAGAGAGCTTG
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/clone="Ulorge="Lung"
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                                                                                              MCCray Lab
University of Iowa
MCCray Lab
University of Iowa
2024 University of Iowa
2024 University of Iowa
2024 University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
(www.openbiosystems.com)
Seq primer: M13 FORWARD
POLYA=Yes:
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TAG TISSUB-Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
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100.0%; Pred. No. ...
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187 c 201 g
                                                                            Contact: McCray, 'PB
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 945)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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TAG TISSUE-grade-2-chondrosarcoma
TAG SEC=ATCTAATATG"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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with a modified polylinker; Plasmid DNA from the
normalized library NOIL CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 110192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
170 c 168 g 79 t ינוסב אסבר אמר Tinear EST 17-JAN-2003, NISC gji3c01.yl NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:3271656 האואת sequence. Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing Center (NISC)
Sequencing Center (NISC)
Clone distribution: NICC)
found through the I.M.A.G.E. Consortium/LLNL at: ö 587 129 707 189 588 ATAGTGCCAGGCTGGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGT 647 708 ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGTGGGCCGCCCCCCTCCTTGCTGGAGG 767 69 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 533)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index TGAACCGGGAGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGG ATAGTGCCAGGCTGGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGT TGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGG 130 GCTACGGCAGCGCGGCGCATGGAGGGCCCCCCCCCCCTACAGCGAGGTCATCGGCC Gaps ö 50.0%; Score 530; DB 14; Length 563; 100.0%; Pred. No. 3.9e-108; Indels , 0 info@image.llnl.gov
Plate: LiAM8009 row: E column: 1
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
1. .563 larity 100.0%; Pred. No. 3.9 Conservative 0; Mismatches organism="Homo sapiens" clone="IMAGE:3271656" /mol\_type="mRNA" /db\_xref="taxon:9606" 757 721 AGAGCAGTGGGCCGCCCTCC 740 CB049800.1 GI:27788087 738 AGAGCAGTGGGCCGCCCTCC Homo sapiens (human) Homo sapiens Unpublished Similarity 5', mkna CB049800 530; 528 10 70 648 Query Match Best Local Matches 52 Bource VERSION KEYWORDS SOURCE ORGANISM BASE COUNT ORIGIN DEFINITION AUTHORS TITLE RESULT 14 CB049800 ACCESSION REFERENCE JOURNAL FEATURES COMMENT ઠે 硆 ઠે 셤 ò 유 ઠે 쉽 8

1007 887 369 827 309 947 370 ceradergaaaagecagaacacrecececrrerragaagagagagagagaagecegee 429 250 GGACCCGGCTCCACCACACACACACCCCCTAGAGAGGGCGCAGCCATCTGGAGAAG 430 GGGGCAGCAAGGCATCGTGTGGCCCTCCCCTCCCCTCTGTGTATAATATTTACAT **ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGGAGG** GGACCCGGCTCCACACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAG AGAAGGATAAACAGAAAAGGACACCTCTCTAGGGTCCCCCAGGGGGGGCCGGGCTGGGGCTG 310 AGAAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCCCGGGCTGGGGCTG CGTAGGTGAAAAGGCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAGGAAGGCGGGG 948 GGCGCAGCAACGCATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTATAAATATTTACAT 1008 GIGAIGICIGALCIGAAIGCACAAGCIAAGAGAGCIIGCAAAAAAAA 1057  844 bp mRNA linear EST 15-JUL-2002 AGENCOURT\_8345390 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6248044 BQ686793 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCS

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clond through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

Hitph-/image-llnl.gov

Plate: LLCM2387 row, e column: 05

High quality sequence stop: 593. BQ686793.1 GI:21812109 Homo sapiens (human) (bases 1 to 844) Homo sapiens Unpublished

/mol\_type="mrm." creticus //mol\_type="mrm." creticus //mol\_type="mrm." creticus //mol\_type="mrm." close="mrm." //mol\_type="mrm." //mol\_type="mrm." //mol\_type="mrm." //mol\_type="mrm." //mol\_orgin="mrm." / 1. .844 /organism="Homo sapiens" Location/Qualifiers

1 others 236 c 239

Length 844; Score 528; DB 13; Pred. No. 7.6e-108; 49.8%; Best Local Similarity

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0;	CGGGA	CGGGA	GCCAG	GCCAG	GGCAG	GGCAG	55555	50000	CGGCT	CGGCT	SGATAA	GATAA	SGTGAA	SGTGAA	PAGCAA	AGCAA	GTCTG	GTCTG		
1; Indels	CAGCTGGAACTGAAC	CAGCTGGAACTGAAC	GACCTGATGGATAG	GACCTGATGGATAGT	AGCGCCACGTGCTAC	AGCGCCACGTGCTAC	GTCATCGGCCACTAC	GTCATCGGCCACTAC	TTGCTGGAGGGGACC	TTGCTGGAGGGGACC	TGGAGCAAAGAGAAC	TGGAGCAAAGAGAAG	GCTGGGGCTGCGTAC	GCTGGGGCTGCGTAC	GAAGGCGGGGGGCG	GAAGGCGGGGGGCG	ATATTTACATGTGA7		AAAA 1061	AAAA 579
Mismatches	GGACCCGAGCAG	GGGACCCCGAGCAG	CCATCTTCGACAGT	CCATCTTCGACAGT	GTAACTCGGGCATC	GTAACTCGGGCATC	CCACCTACAGCGAG	CCACCTACAGCGAG	STGGGCCGCCCTCC	greecceccrcc	AGAGCGCAGCCATC	AGAGCGCAGCCATC	CCCAGGGGGGCCGG	CCAGGGGGGCCGG	AAGAGGAGTGAGAG	aagaggagtgagag	CTCCCTGTGTATAA	CTCCCTGTGTATAA	TGCAAAAAAAAAA	I GCAAAAAAAAAA TGCAAAAAAAAAA
0	GCTTC	GCTTC	CAGAA	CAGAA	CAGCA	CAGCA	00000	90000	GAGCA	GAGCA	CCTAG	CCTAG	GGGTC	GGGTC	CTTAG	CTTAN	CCCAC	CCCAC	GAGCT	GAGCT
. Conservative	GCCCCTGCACCTTCGGGACCCCGAGCAGCTGGAACTGAACCGGGAGTCGG	GCCCCTGCACCCTCCAGCTTCGGGACCCCCGAGCAGCTGGAACTGAACCGGGAGTCGG	TGCGCGCACCCCCAAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGG	TGCGCGCACCCCCAAACAGAACCATTCGACAGTGACCTGATGGATAGTGCCAGGCTGG	GCGGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCG	GGGGCCCCTGCCCCCCCAGGAGTAACTCGGGCATCAGGGCCCACGTGCTACGGCAGGGCG	GGCGCATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCT	GGCGCATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCT	CCTTCCAGCACCAGCAGTGGGCCGCCCTCCTTGCTGGAGGGACCCGGCTCCACC	CCTTCCAGCACCAGCAGAGCAGTGGCCGCCCTCCTTGCTGGAGGGGGACCCGGCTCCACC	ACACACACACATGGGCCCCTAGAGAGGGCGAGCCATCTGGAGGAAAAGAGATAAACAGA	ACACACACATGGGGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGGATAAACAGA	AAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGCTGCGTGAAAAGGC	AAGGACACCCTCTCTTTTTTTTTTTTTTTTTTTTTTTTT	HGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAAGGAGGGGGGGG	HILLINIA BERAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CGTGTGGCCCTCCCCACCTCCTGTGTATAAATATTACATGTGATGTCTGGTCTG		AATGCACAAGCTAAGAGAGCTTGCAAAAAAAAAAAAAAA	AATGCACAAGCTAAGAGAGCTTGCAAAAAAAAAAAAAAA
578;	483 (	Н	543	61	603	121	663 (	181 (	723	241	783	301	843	361	606	421	963	481	1023	541
Matches	δ	qq	<b>%</b>	QQ	ò	Db	λΌ	Db	λ̈́o	qu	λο	Db	ò	qu	ò	qq	ò	ନ୍ଧ	ò	qa

Search completed: December 8, 2003, 06:17:44 Job time : 2648 secs ٠,۶

b-44.rng

# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

December Run on:

7, 2003, 21:17:14; Search time 344 Seconds (without alignments) 8325.883 Million cell updates/sec

US-09-857-826B-44

Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2552756 segs, 1349719017 residues Searched:

Total number of hits satisfying chosen parameters:

5105512

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N Geneseq 19Jun03:\*

| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
| SIDSI/gcgdata/geneseqfy-embl/NA1981.DAT:\*
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| SIDSI/gcgdata/geneseqfy-embl/NA1999.DAT:\*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT: /SIDS1/gcgdata/geneseq/gensequ-embl/NA2001B.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\* 22011154

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					•				
	Description	Sequence encoding	Human secretory po	Prostate cancer-as	Human polynucleoti	Human polynucleoti	cDNA encoding a hu	cDNA clone encodin	cDNA clone encodin
	ID		ABZ36103	ABK92120	AAI57868	AA159654	AAA75151	AAA75163	AAA75164
	DB	21	25	24	22	22	21	21	21
	Match Length DB	1061	1334	1140	1066	1069	696	696	696
% Query	Match	100.0	99.7	97.5	96.2	93.4	7.06	90.5	90.5
	Score	1061	1057.8	1034.4	1021.2	991.2	961.8	960.2	960.2
Result	No.		~	m	4	υ Ω	9	7	80

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	עכ	300.7	30.5	464	77	AAA/5165	CDNA CIONE encogin
	10	9.008	75.5	1321	24	ABK12137	Human cDNA encodin
	11	728.8	68.7	1583	24	ABS61424	Prostate specific
O	12	644.2	60.7	693	24	ABK12143	Human MIVR-1 homol
	13	523.8	49.4	878	24	ABK12142	Mouse cDNA encodin
	14	521.4	49.1	1713	21	AAA75152	cDNA encoding a mu
	15	519.8	49.0	1713	21	AAA75166	cDNA clone encodin
	16	519.8	49.0	1713	21	AAA75167	cDNA clone encodin
	17	519.8	49.0	1713	21	AAA75168	cDNA clone encodin
	18	477.8	45.0	1879	23	AAS84503	DNA encoding novel
, ,	19	418.6	39.5	474	25	ABZ84732	Toxicologically re
	20	399.8	37.7	408	22	AAF65983	Novel human polynu
	21	399	37.6	673	24	ABT09178	Phase-1 Rat CT gen
	22	365.6	34.5	812	20	AAZ52964	Human prostate tum
	23	352.4	33.2	937	21	AAZ52507	Human secreted pro
	24	350.8	33.1	920	24	ABK34251	Human cDNA for nov
	25	350	33.0	8093	24	ABK12145	Human MIVR-1 homol
	56	349	32.9	8494	23	AAS77304	DNA encoding novel
	27	345.8	32.6	8065	19	AAV38335	Manic-depressive i
υ	28	334.8	31.6	8103	23	AAS77312	DNA encoding novel
	59	281	26.5	8440	23	AAS77305	DNA encoding novel
	30	281	26.5	8440	24	ABK83477	Human cDNA differe
	31	277.8	26.2	8011	13	AAV38336	Manic-depressive i
	32	253.6	23.9	8041	23	AAS77310	DNA encoding novel
	33	249.2	23.5	475	24	ABK12144	Human MIVR-1 homol
	34	239.4	22.6	426	23	AAS84502	DNA encoding novel
	35	232	21.9	254	21	AAA41265	Human secreted exp
	36	223.4	21.1	1428	23	AAS92497	DNA encoding novel
	37	223.4	21.1	2942	23	AAS77313	DNA encoding novel
	38	188.4	17.8	522	24	ABT10027	Human breast cance
	39	9	5.7	9	24	ABN40872	Human spliced tran
	40	52.8	•	114955	20	AAX53491	Human adenosine Al
	41	51	4.8	51	22	AAH89714	Human coding sequ
	42	48.4	4.6	1337	20	AAZ17263	Human gene express
O	43	48.4	4.6	0	22	AAL03113	Human reproductive
	44	48.2	4.5	336	24	ABS54598	DNA encoding varia
O	45	48	4.5	114955	20	AAX53491	Human adenosine Al

### ALIGNMENTS

AAA47429 standard; DNA; 1061 BP. 20-OCT-2000 (first entry) AAA47429; RESULT 1 AAA47429 

Sequence encoding human neuron-associated protein.

Meuron associated protein, NEUAP; neurological disorder; epilepsy; stchemic carebrovascular disease; stroke; cerebral neoplasm; stchemic carebrovascular disease; stroke; cerebral neoplasm; Alzheimer: & disease; Pick's disease; Huntington's disease; meningitis; modementia; Parkinson's disease; demyelinating disease; meningitis; prion disease; kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy; muscular dystrophy; central nervous system; CNS; we peripheral nervous system; PNS; myopathy; schizophrenia; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD; autoimmune disease; inflammation; acquired immunodeficiency syndrome; albeigh, addison's disease; adult respiratory distress syndrome; albeigh; analergy; ankylosing spondylitis; amyloidosis; anaemia; asthma; we wener syndrome, trauma; human; ds.

Homo sapiens

Location/Qualifiers 101..859 Key

/\*tag= a /product= Neuron associated protein

98US-9123456. 99US-0119365. 99WO-US30408 99US-0124687 WO200034477-A2 11-DEC-1998; 16-MAR-1999; 10-DEC-1999; 15-JUN-2000 11-DEC-1998

(INCY-) INCYTE PHARM INC

Yang J; Lal P, Au-young J, Hillman JL, Baughn MR, Yue H, B Azimzai Y; YT, Tang YT, Lu DAM,

WPI; 2000-423423/36. P-PSDB; AAB01388.

New human neuron-associated proteins and polynucleotides encoding them, useful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders

9; Page 136; 145pp; English. Claim

treating or preventing a disorder associated with decreased expression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NeUAP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic or activity of NEUAP. NEUAP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, Huntington's disease, dementia and Parkinson's disease, Huntington's disease, dementia and Parkinson's disease. NEUAPS are also useful for treating other demyelinating diseases. NEUAPS are also useful for treating other cerebrough and viral meningitis, prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and metabolic diseases of the nervous system, neurofibromatosis, other developmental disorders of the central nervous system disorders, plass, neuroskeletal disorders, autonomic nervous system disorders, creanial nervous system disorders, cranial nervous system disorders, inherited, metabolic, endocrine, and toxic myopathies, mental other metabolic, endocrine, and toxic myopathies, mental disorders including mood, anxiety and schizophrenic disorders, creative disorders, bursitis, cirrhosis, paroxysmal nocturnal heamoglobinuria, cancers of the adrenal gland, bladder, bone, tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal heamoglobinuria, cancers of the adrenal gland, bladder, bone, tissue disease, dault respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anethal werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, unifications, and trauma. This sequence was given the Incyte ID no. 

Seguence 1061 BP; 225 A; 342 C; 326 G; 168 T; 0 other;

Query Match

120 120 180 9 9 TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGTTCAGTGGGCCATGATCCCCGAGCTGC TGGAGAACTGAAGGCGGACGGTCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGT TCAGATCATCATCATCGTGGTGGTGATGATGATGATGATGGTGGTGGTGATCACGTGCTGCT TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGGTTCAGTGGGCCCATGATCCCCGGAGCTGC Gaps 0; Indels 4.5e-220; . 100.0%; Score 1061; 100.0%; Pred. No. 4.5 :ive 0; Mismatches Best Local Similarity 100. Matches 1061, Conservative ч 61 121 요 ò 엄 ઠે 8

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DB 21; Length 1061;

1020 ATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTATAAATATTTACATGTGATGTCTGGTC 1020 TCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGATCACGTGCCTGCT 180 300 300 360 360 420 420 480 480 540 540 600 900 9 999 720 720 780 780 840 840 900 900 960 960 GAAAGGACACCCTCTTTAGGGTCCCCAGGGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAG GAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGGAGGAG GAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGAGGAG AGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACACTGTCTCAGGCAA GGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTC CGGCGCATGGAGGGCCGCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGGTC CTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCA CTCCTTCCAGCACCAGCAGAGCAGTGGGCCCCCCTCCTTGCTGGAGGGGACCCGGCTCCA CCACACACACACTCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACA GAAAAGGACACCTTCTCTAGGGTCCCCAGGGGGCCCGGGCTGGGGCTGCGTAGGTGAAAAG AGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAA GCCCTTCGCCCAGCGCAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCA coagarcoroccoccoccarcrocrororogacococaoccoccoccarcora 541 GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT GGGCGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAGCGG CGGGCGCATGGAGGGCCGCCGCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC CCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACA GCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAGGAAGGCGGGGGGCGCAGCAACGC GCAGAACACTCCGCGCCTTCTTAGAAGAGGAGTGAGAGGAAAGGCGGGGGGGCGCAACGC ATCGTGTGTGCCCCCCCCCCCCCCCCCCTGTGTATAAATATTTACATGTGATGTCTGGTC GCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCA <u> GGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTC</u> GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT 1061 BP. ABZ36103 ID ABZ36103 standard; cDNA; 1334 1021 241 361 481 781 841 901 961 1021 ABZ36103; 181 181 241 301 301 361 421 421 541 601 721 781 841 901 961 481 109 661 661 721 RESULT ò g ò 셤 ò g ò g ò g ò g ò ద δ d ð 셤 ò 셤 ò g ò 셤 8 g ò 셤 ò g

õ Human secretory polynucleotide SPTM SEQ ID (first entry) 10-FEB-2003 XBXBXBX

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Dec Tue

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anaemia;
Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia, asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer, disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; neuropetic; antisonvulsan; cytoetatic; antisparkinsonian; arxiolytic; secretory polynucleotide; secretory protein; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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WO200283876-A2

24-OCT-2002

27-MAR-2002; 2002WO-US09921

29-MAR-2001; 2001US-280067P.
29-MAR-2001; 2001US-280068P.
16-MAY-2001; 2001US-291280P.
17-MAY-2001; 2001US-291849P.
19-UN-2001; 2001US-299428P.
20-UM-2001; 2001US-299428P.

(INCY-) INCYTE GENOMICS INC

Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J, Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR; Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B; Flores V, Marwaha R, Lo A, Lan RY, Urashka ME; 

田;

2003-075543/07.

P-PSDB; ABP75660

New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or cancers

Claim 1; SEQ ID NO 267; 458pp + Sequence Listing; English.

The invention relates to a secretory polynucleotide (designated sptm)

Comprising any of 567 polynucleotide sequence at least 90 % identical to

combinately occurring polynucleotide sequence at least 90 % identical to

the polynucleotide sequence, a polynucleotide complementary to them or an

CC the polynucleotide sequence, a polynucleotide are useful for

RNA equivalent of them. The polypoptide or polynucleotide are useful for

CC tracting, preventing or diagnosing a disease or condition associated with

CC diagnosing, treating or preventing autoimmuse/inflammatory disorders

CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,

CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,

CC multiple sclerosis, cerebral palsy, Parkinson's disease,

CC multiple sclerosis, cerebral palsy, Parkinson's disease,

CC schizophrenia or amnesia), or cell proliferative disorders (e.g.

C psoriasis, polycythemia vera, or cancers including adenocarcinoma,

CC breast, cervix or prostatel)

CC breast, cervix or prostatel

CN oce: The sequence data for this patent did not form part of the brain,

CN oce: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO at

Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 other;

ö 9 1 TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGTTCAGTGGGCCCATGATCCCCGAGCTGC Gaps ö DB 25; Length Score 1057.8; DB 25; Lengt Pred. No. 2.3e-219; 0; Mismatches 2; Indels 99.7%; Matches 1059; Conservative Local Similarity

ò g

ABK92120 ID ABK9 9 TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGGTTCAGTGGGGCCATGATCCCCGAGCTGC

1020 240 240 300 300 360 420 420 480 480 540 600 600 999 999 720 720 780 780 840 840 960 CGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC GAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAG GAGCCACTACAAGCTGTCTGCACCGTCCTTCATCAGCCGGCACGCCAGGGGCGGGAGGAG AGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACACTGTCAGGCAA GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT GGGGGGCCCCTGCCCCCCCGGGGTAACTCGGGCATCAGCGCCCACGTGCTACGGGCG CTCCTTCCAGCACCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCA CCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGGATAAACA CCACACACACATCGCGCCCCTAGAGAGCGCACCATCTGGAGCAAGAGAAGAAGATAAACA GAAAGGACACCCTCTCTAGGGTCCCCAGGGGGCCGGGCTGGGCTGCGTAGGTGAAAAG ATCGTGTGGCCCTCCCTCCCTCCCTGTGTATAAATATTTACATGTGTGTCTGGTC Arcereresecerecereceaecrecereseranaararraacarereaecresere rcadarcarcarcarceregregreargargargargeregregrearcacerecrecr GAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGGGGGAG AGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAA GCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCA CGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCCTACCA GGGCCCCTGCACCCTCCAGCTTCGGGACCCCCGAGCAGCTGGAACTGAACCGGGAGTC GGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTC GGGCGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGG CGGGCGCATGGAGGGGCCGCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC CTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCA GCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAGGAAGGCGGGGGGGCGCAGCAACGC TCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGCT GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT 241 541 1021 61 121 181 181 241 301 301 361 361 421 481 481 721 781 781 841 901 901 961 961 121 421 541 601 601 661 721 841 61 661 8 6 g 셤 ò 셤 ò 셤 ò 셤 ò g ð g ò g ò 셤 ò 임 ò g ò g ò g ò g 8 g ò ò ò

RESULT 3

ABK92120 standard; DNA; 1140

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer. The nucleic acid sequences are particularly useful
                                                                                        Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for diagnosing or treating prostate cancer, as well as foi identifying modulators of prostate cancer or agents that inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Hevezi P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1034.4; DB 24
Pred. No. 2.6e-214;
0; Mismatches 6;
                                                              DNA sequence
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2000US-0733288.
2000US-0733742.
2001US-263957P.
2001US-276791P.
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2001US-281922P.
2001US-286214P.
2001US-0847046.
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99.2%;
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                                                              Prostate cancer-associated
                                     (first entry)
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P-PSDB; ABG61805.
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30-APR-2001;
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                                                                                                                     AGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGGGCACAGTGTCAGGCAACGG
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                                 GATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAG
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AAI57868 standard; cDNA; 1066 AA157868; RESULT 4
AAI57868
ID AAI5
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AC AAI5

AGAACTGAAGGCGGACGGTCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGGTTTGTTCA 123

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TCCTTGGGTTCGGGTGAAAGCGCTTGGGGGTTCAGTGGGCCCATGATCCCCGAGCTGCTGG

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Indels

Best Local Similarity 99.2 Matches 1050; Conservative

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TCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGCT

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GAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGGAGGAG

249 AGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAA

309 cegaarcecadadecedeadereracececedececeaeceaeceaeceredecerece GCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCA

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GGGCCCCTGCACCTCCAGCTTCGGGACCCCCAAGCAGCAGCTGGAACTGAACCGGGAGTC

GGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCTGGAACTGAACCGGGAGTC

GCCCTTCGCCCAGCGGGAGCGCTTCCACCCCTTCCAGCCCTATCCGTACCTGCAGCA

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CGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC

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GGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGGGCCTGATGGATAGTGCCAGGCT GGGCGCCCCCCCCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGG

GGTGCGCGCACCCCCAAACAGAACCCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT

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CCACACACACATCGCGCCCCTAGAGAGCGCGAGCCATCTGGAGGAAAGAGATAAACA GAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGTTGCGTAGGTGAAAAG

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CTCCTTCCAGCACCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCA

GAAAGGACACCCTCTTAGGGTCCCCAGGGGGCCGGGCTGGGGCTGCGTGAAAG

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                                        Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scletcosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                    Wang
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Yang Y,
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u C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                  Chen R,
                                       nootropic; immunosuppressant;
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                    Human polynucleotide SEQ ID NO 71.
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Wehrman T, Xu
Goodrich R, D
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03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
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09-JUL-2000; 2000US-0598042
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Wang Z, W
Zhou P,
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                                                                                        leukaemia; ss
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The invention relates to human nucleic acids (AAI57788-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous asystem diseases, such as Alzhelmer's, Parkinson's disease, Huntington's disease, anyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemclatic/chemckinetic activity, haemotactic/chemckinetic activity, haemotactic/and inflammation, leukaemias and The sequence data for this patent did not form part of the printed

120 9 75 TCCTCCTTGGGTTCGGGTGAAAGCGCTTTGGGGGTTCAGTGGGCCATGATCCCCGAGCTGC TGGAGAACTGAAGGCGGACGGTCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGT 7; Gaps Score 1021.2; DB 22; Length 1066; Pred. No. 1.8e-211; 0; Mismatches 8; Indels 7; 96.2%; Query Match
Best Local Similarity 98.6
Matches 1043; Conservative 16 61

AAIS9654 standard; cDNA; 1069 22-OCT-2001 (first entry) AA159654; RESULT 5
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                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Humtington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                     Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1054 TCCTCCTTGGGTTCGGGTGAAAGCGCTTGGGGGGTTCAGTGGGCCCTGATCCCCCGAGCTGC
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Zhang J
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Yang Y,
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Pred. No. 5.7e-205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3643; 10078pp; English.
Human polynucleotide SEQ ID NO 3643.
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llarity 97.8%;
Conservative (
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
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03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
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29-NOV-2000; 2000US-0727344
                                                                                                                                                                                      26-DEC-2000; 2000WO-US34263
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P-PSDB; AAM40498.
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Matches 1037; Conserv
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                                                                                    leukaemia; ss
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                                       GAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCA
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ID AAA75151

XX AAA75151;

XX XX AAA75151;

XX XX CONN (first entry)

XX XX CONN encoding a human TANGO 261

XX XX
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b-44.rng

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Query Match
Best Local Similarity 99.8%;
Matches 963; Conservative
                                                                         WPI; 2000-579269/54.
                                                                           P-PSDB; AAB18449
                                                            01-MAR-1999;
                        sapiens
                                                    08-SEP-2000
                                     sig_peptide
                                         mat_peptide
                                                                                  262,
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The present sequence encodes a human TANGO 261 polypeptide. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. TANGO 267, and TANGO 267. TANGO 267, and and the TANGO 1010 and of the TANGO 261 and the TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. TANGO 267. 
TANGO 266; TANGO 216;; TANGO 261; TANGO 267;

cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atlectasis; pulmonary congestion;
oedema: emphysema: chronic bronchitis; bronchial aschma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
ardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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Pred. No. 1.3e-198;
0; Mismatches 2; Indels 0;
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6.764 a
/trag= a /product= "TANGO 261"
6.89 b
/trag= b
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                                                              GGTGGTGATCACGTGCCTGCTGCTGACAAGCTGTCTCGCACGGTCCTTCATCAG
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AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO copypeptides can be used to modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, requlate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation in proliferation, and/or function of cells that appear in the bone matrow, and leukocytes, treat bone matrow, blood and hematopoietic associated diseases and disorders, atlectasis, bronchial and bronchiectasis, intestinal disorders, spleen associated as shown and bronchiectasis, intestinal disorders, spleen associated as schemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral control of bone and cartilage cells and to treat bone and/or treat disorders associated with the ovaries, and cerebral control of bone and cartilage cells and to treat bone and/or treat disorders associated with the ovaries, and cerebral control of bone and cartilage cells and to treat bone and viral meningits, Alzheimer's Disease, inflammations, bacterial and viral meningits, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.
                                                                                                                            TANGO 266; TANGO 216;; TANGO 261; TANGO 267;

cellular proliferation; cellular differentiation; cellular adhesion;

von Willebrand factor-associated disorder; cell trafficking; cancer;

hematopoietic associated disease; atlectasis; pulmonary congestion;

oedema; emphysema; chronic bronchitis; bronchial aschma; bronchiectasis;

intestinal disorder; spleen associated disease; renal disorder;

ardiovascular disorder; ischemic heart disease; hydrocephalus;

brain herniation; iatrogenic disease; inflammation; meningitis;

Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;

multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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e.g. for treating cancer -
                                                                                       clone encoding a human TANGO 261 polypeptide.
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Created using information provided.
                                                                                                                                         cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; brain charge inflammation; iatrogenic disease; inflammation; meningitis; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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                                             DB 21; Length 969;
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Sequence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 other;
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M
                                       Score 960.2; DB 21
Pred. No. 2.8e-198;
0; Mismatches 3;
                                       90.5%;
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                                                               Similarity
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that appear in the bone marrow, and leukocytes, treat bone marrow, and hematopoietic associated diseases and disorders, atelectasis, and hematopoietic associated diseases and disorders, atelectasis, audimonary congestion or cedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, splen associated diseases, modulate rena cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.
                                                                                                                                                                                                                               cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular marrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA75163-65 encode human TANGO 261 proteins. The specification also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                     cDNA clone encoding a human TANGO 261 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "TANGO 261"
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6..764
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                                          AAA75165 standard; cDNA; 969 BP.
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P-PSDB; AAB18463.
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note: the present sequence does not appear in the specification; it was created using information provided.
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                                                                       21; Length 969;
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                                          Seguence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 other;
                                                                      Score 960.2; DB 21
Pred. No. 2.8e-198;
0; Mismatches 3;
                                                                       90.5%;
                                                                                                       Matches 962; Conservative
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Best Local Similarity
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specifically claimed in claim 3"
                                                                                                                                                                                           cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis; heart failure.
                                                                                                                                                                  Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid molecule encoding Mechanically Induced Vascular
Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                                                                                                                                                    gene; MIVR-1; Mechanically Induced Vascular Receptor
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                                                                                                                                                                                                                                                                                             note= "This region is
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                                                                                                                                                                                                                                                                                                                                                                                                                Kennedy SP,
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                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                    "MIVR-1"
                                                                                                               BP.
h7:50:11 2003
                                                                                                               standard; cDNA; 1321
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Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
Cardiac cell anti-apoptotic activity and fragments of it provided
they are not identical to Genbank sequences AI761441.1, AI594390,
Chey are not identical to Genbank sequences AI761441.1, AI594390,
Chey are not identical to Genbank sequences AI761441.1, AI594390,
Chey are not identical to included are expression vectors, host
cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of
MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity
with a candidate agent, where the molecule is a nucleic activity is
comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its
comprising MIVR-1, determining if the anti-apoptotic activity is
modulated and thereby identifying a modulator. The cardiac cell antiapoptotic molecules and mucleic acids of the invention are useful for
treating, diagnosing and monitoring progression of such diseases and
disorders as characterised by increased apoptotic cell-death of vascular
condothelial cells e.g. cardiac hypertrophy, myocardial infarction,
stroke, arteriosclerosis and heart failure. The present sequence encodes human MIVR-1.

Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 other;

ö Gaps 75.5%; Score 800.6; DB 24; Length 1321; 98.3%; Pred. No. 9.8e-164; ive 0; Mismatches 14; Indels 0; Conservative Best Local Similarity Matches 809; Conserv Query Match

1158 1218 979 AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGCGGCCCCCTGCCCCCCGG 1038 1039 CAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGGGGCGCTTGGAGGGGCCGCC 1098 141 558 201 618 261 678 321 738 381 798 441 828 501 918 561 978 621 681 741 861 1099 GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACACAGAGG ACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGA 802 AGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAAGG AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGT CTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCG craceccceccrosecccaccsaccsccresecsresecsccrroseccassess CTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCAC 859 carcicocrorcadacocodos acececenaceas de consecuentes es co AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCCAG 682 GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAG rrrerrccagaccarccagacrcccagacrccacrtrrcrrcagarcarcarcarcarcar GGTGATGATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC CATCTCGCTGTCAGACGGGGAGGACCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT CAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCCATGGAGGGGGCCCCC TCCCCAGGGGGCCGGGCTGGGCTGCGTAGGTGAAAAGGCAG 1321 TCCCCAGGGGGCCGGGCTGGGGTGAAAAGGCAG 904 262 799 622 742 1279 619 739 562 619 382 502 862 82 499 142 322 442 Ω 셤 셤 g 임 요 a ò g g g 원 ò ò ઠે g ò ò 용 ò 셤 8 ò ò ò ò ઠ

ABS61424 standard; cDNA; 1583 RESULT 11 

ABS61424;

BP.

(first entry) 05-NOV-2002

Prostate specific nucleic acid DEX0259\_32

Human; ss; prostate specific nucleic acid; PSNA; prostate cancer; cytostatic; non-cancerous prostate disease; PSP; vaccine; prostate specific protein; metastasis.

Homo sapiens

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WO200216416-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide comprising a sequence with 60 % identity to one of prostate specific protein (BSP) sequences. Or comprising an amino acid sequence encoded by one of 136 nucleotide prostate specific nucleic acids sequence. PSNA, (or a sequence that bybridises to it or is 60% identical to it), given in the specification. Also included are a vector comprising the polynucleotide, a host call comprising the vector, an antibody specific for the PSP proteins and a vaccine comprising the protein or polynucleotide. The PSP and PSNA are useful for diagnosing and annitoring the presence and metastases of prostate cancer in a patient. The PSNA is useful for determining the presence of prostate cancer, which induces an immune the level PSNA in a sample. An antibody to the PSP is useful for determining the presence of prostate cancer, which induces an immune response against the prostate cancer call expressing the nucleic acid or polypeptide and a kit is useful for detectining a risk of cancer or presence of cancer in a patient. PSNA is useful as hybridisation probes to detect, characterise and quantify hybridising nucleic acids from both microarrays. Sequences of PSP and PSNA are useful as components in microarrays. Sequences of PSP and PSNA are useful as components in a patient.
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                                                                                                                                                                                                         New polypeptide useful for diagnosing and monitoring the presence metastases of prostate cancer in a patient and as a component in databases for search analysis as well as in sequence analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to drive in vivo expression of PSP. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1583 BP; 361 A; 469 C; 457 G; 296 T; 0 other;
                                                                                                                                                                                                                                                                               Claim 1; Page 166-167; 242pp; English.
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thompson JF,
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(first entry)

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NW 004338 and AQ177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule expression product. determining if the anti-apoptotic activity is expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and alsorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence is one of the four Genbank sequences (AI764141.1) which are homologous to the cDNA for human MIVR-1 and which are specifically disclaimed. 418 CGCATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTATAAATATTTACATGTGATGTCTG 1017 634 658 478 718 577 457 397 337 777 277 837 217 897 157 957 97 96 cecarcererecerecereceaecrecerereraraararraearerearerere 37 CACGAGATCGA-CTGCCGCCCACCATCTCGCTGTCAGACGGG--AGGAGCCCCCACCCTAC TCGGTGCGCGCACCCCCCAAACAGAACCATCTTCGACAGGGGACCTGATGGATAGTGCCAGG CTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGC TCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGGGGACCGGGTT CCCCCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAGAAGAAGAAGAAAAA CCGCCCTTCGCCCAGCGGGAGCGCTTCCACCCTTCCAGCCCACCTATCCGTACCTGCAG 693 CCGCCTTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACNTGCAG CAGGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAG TCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGG CTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAGC GGCGGCGCATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGG TCCTCCTTCCAGCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGA-GGGGACCCGGCT CCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGATAA ACAGAAAGGACACCCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGCTGCGTAGGTGAA ACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGCTGCGTAGGTGAA AAGGCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGAGAGGAAGGCGGGGGGGCGCAGCAA **AAGGCAGAACACTCCGCGCGTTCTTAGAAGAGGAGTGAGAGGAAGGCGGGGGGGCGCAGCAA** 4; Gaps Query Match 60.7%; Score 644.2; DB 24; Length 693; Best Local Similarity 98.1%; Pred. No. 5.7e-130; Matches 683; Conservative 0; Mismatches 9; Indels 4; Sequence 693 BP; 101 A; 205 C; 237 G; 149 T; 1 other; GTCTGAATGCACAAGCTAAGAGAGCTTGCAAAAAA 1053 GTCTGAATGCACAAGCTAAGAGAGCTTGCAAAAAAA 599 1018 359 419 633 479 576 539 516 456 629 396 719 778 276 838 216 898 156 928 음 g 윱 a g 셤 셤 ò 셤 ઠે g ઠે g ઠ g ઠે ઠ ŝ ઠે ઠે δ ò ò

Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having advancially Induced Vascular Receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences A176141.1, A1594390, and 004338 and AQ177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic activity is comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic and thereby identifying a modulator. The cardiac cell anti-apoptotic and thereby identifying a progression of such diseases and disorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, etroke, arteriosclerosis and heart failure. The present sequence 153 154 AGTGATGATGGTGATGGTGGTTATGATTACGTGCCTGCTGAGGCCACTACAAGCTGTGACAGC 213 94 TTTGTTCCCCAGCATGGAGATCACGGAGCTGGAGTTCGTGCAAATCGTGGTCATCGTGGT 142 GGTGATGATGGTGATGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCGACTACAAGCTGTCTGC TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT Mouse; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis; heart failure. Gaps Mouse cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1 Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases 27; Score 523.8; DB 24; Length 878; Pred. No. 6.5e-104; 0; Mismatches 117; Indels 27; ĮĞ, Turi Sequence 878 BP; 179 A; 305 C; 247 G; 147 T; 0 other; Thompson JF, Disclosure; Page 99-100; 105pp; English BRIGHAM & WOMENS HOSPITAL INC. PFIZER INC. Kennedy SP, Location/Qualifiers 20..844 /product= "MIVR-1" 49.4%; 81.9%; 21-AUG-2001; 2001WO-US26089. 22-AUG-2000; 2000US-227159P Jest Local Similarity 61.7 Matches 651; Conservative Landschulz KT, encodes mouse MIVR-1. WPI; 2002-280912/32. P-PSDB; AAU78236 WO200216416-A2. Mus musculus. 82 Lee RT, (BGHM) (PFIZ Key a 요 ŝ ò

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ABK12142 ID ABK12142 standard; cDNA; 878

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Pred. No. 2.5e-103;
0; Mismatches 151; Indels 42;
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/product= "TANGO 261"
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P-PSDB; AAB18450.
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15 297 120 357 60 Gaps 42; DB 21; Length 1713; Indels Score 519.8; DB 21; Pred. No. 5.5e-103; 0; Mismatches 152; Fraser CC; Sharp JD,

> encoding a murine TANGO 261 polypeptide. BP AAA75166 standard; cDNA; 1713 (first entry) 15-JAN-2001 cDNA clone AAA75166; RESULT 15 AAA75166 ID AAA75

TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atlectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

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AAA75166-68 encode murine TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO 269 boltypeptides can be used to modulate cellular spoiliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation differentiation, and/or function of cells that appear in the bone marrow, and leukocyes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchic asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. How may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, barkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders creating in twas contact the present sequence does not appear in the specification; it was contact and corpus or and treat hepatic disorders. Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -Sequence 1713 BP; 505 A; 439 C; 400 G; 369 T; 0 other; Disclosure; Page -; 175pp; English. created using information provided. / Match 49.0%; Local Similarity 78.4%; Les 703; Conservative 0 (MILL-) MILLENNIUM PHARM INC 99US-0122458 01-MAR-2000; 2000WO-US05226 DA, Holtzman WPI; 2000-579269/54. P-PSDB; AAB18464 01-MAR-1999; Barnes TM, 358 121 Query Match Best Loca Matches e.g. ò 원 ò g ò 셤 셤 ò

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GTGGGTGGGGGACCCCG	CGGCGGGCGCATGGAGGG 	CCACCACACACATCGCGCCCCTAGAGA	AAGGCAG
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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2888711 seqs, 20454813386 residues Searched:

5777422 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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GenEmbl:\* Database :

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	cription		28643 1	15918	05616 1	117	119 8	AF305426 Homo sapi	341 Human	522	130	3995 Mus mu	2821	ALB37509 Mouse DNA	Mile OC	208 Mus	117 Ratt	378 Rattus	267 Sequenc	AX525744 Sequence	109 Sequenc	13 Sequence	328 Homo Ba	32 Sequence	AF009426 Homo sapi	884 Sequenc	883 Seque	AFOO9424 HOMO BADI	385 Seque	lomo sa	3425 Homo	Omo!	Olo Homo	OHO.	131 Sequence	Mus m	ood Rattus	364 Ratt	1069 Mus mu	5347 Dani	34911 Mus mus	28820 Zebraf	21913 Human DN	609	
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## ALIGNMENTS

	linear PRI 18-JUL-2000	complete cds.					
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r 1 278		DEFINITION	_	VERSION	KEYWORDS	SOURCE	ORGANISM

Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1141)
Xu,L.L., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G.,
Moul,J.W. and Srivastava,S.
A novel androgen-regulated gene, PMEPA1, located on chromosome

REFERENCE AUTHORS

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AY128643.1 GI:22121998
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E 2 (bases 1 to 1141)
S Xu,L.L., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLv, Molly,J.W. and Silvastava,S.
Direct Submitssion
AL Submitted (12-JAN-2000) CPDR, USUHS, 1530 East Jeffers Rockville, MD 20852, USA
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ND 20852, USA
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/ Accation/Qualifiers
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/ Chromosome="120"
/ Ab xref="taxon:9606"
/ Chromosome="120"
/ Ab zef="120413.31-13.33"
/ Cell line="LNCap"
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אוזבסט 1818 bp mRNA linear PRI 10-APR-2003
Homo sapiens PMEPAl variant A protein mRNA, complete cds.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Submitted (03-JUL-2002) Department of Medicine, Case Western Reserve University, Howard Hughes Medical Institute, 11001 Cedar Ave., Cleveland, OH 44106, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTC
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840 839 900 960

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: e Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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Homo sapiens, clone MGC:20374 IMAGE:4559576, mRNA, complete cds.
BC015918
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1 (bases 1 to 1061)
Strausberg,R.
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Submitted (15-007-201) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                              840 GAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGGCTGGGGCTGCGTAGGTGAAAAG
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Contact: MGC help desk
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Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Score 1032.2; DB 9; Length 1818;
Pred. No. 2.3e-184;
0; Mismatches 3; Indels 7;
                                                                                                                                                      /codon_start=1
|product== MBFBAl variant A protein"
|protein_id="AAM89277.1"
|db_xref="GI:22121999"
                                                                                                                                                                                                                                                                                                                                 398
                                      organism="Homo sapiens"
                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                /map="20q13.31-13.33"
                                                                                                                                                                                                                                                                                                               LESAAIWSKEKDKQKGHPL"
location/Qualifiers
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                                                                                              chromosome="20"
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Best Local Similarity 99.1%;
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/product="Unknown (protein for MGC:20374)"
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/db_xref="G1:16198475"
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                                                                                                                                                                                                                                                                                                                                                                                                        90.3%; Score 957.6; DB 9; llarity 98.6%; Pred. No. 2.6e-170; Conservative 0; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                   161
lib="NIH_MGC_14"
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Matches 966; C
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YQGPCTLQLRDPEQQLELNRESVRAPPNRT I FDSDLMDSARLGGPCPPSSNSGI SATC
YGSGGRMEGPPPTYSEVI GHYPGSSFQHQQSSGPPSLLEGTRLHHTHI APLESAAI WS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4839)
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TCCCCAGGGGGGGGGGGGTGGGTGGGTGAAAAGGCAGAAAAACACTCCGCGCTTCTT
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                                                                                                             TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGGATCATCATCATCGTGGT
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Mol. Carcinog. 32 (1), 44-53 (2001)
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Rae,F.K., Hopper,J.D., Nicol,D.L. and Clements,J.A.
Direct Submission
Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane,
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Pred. No. 4.8e-170;
); Mismatches 15;
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Homo sapiens STAG1/PMEPA1 mRNA,
AF305616
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321. .1184
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Location/Qualifiers
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Euteleostomi;

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larity 98.3%; Pred. No. 9.3e-141;
Conservative 0; Mismatches 14; Indels 0;
                                              Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. Turi, T.G.
Diagnosis and treatment of cardiovascular conditions
Patent: WO 0216416-A 1 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER IN
Location/Qualifiers
               Craniata; Vertebrata; E
Catarrhini; Hominidae;
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               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Turi, T.G.
Diagnosis and treatment of cardiovascular conditions
Patent: WO 0216416-A 3 28-FEB-2002,
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC.
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    /note="unnamed protein product"

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Submitted (1J-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 61505)
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Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
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/orl.type="genomic DNA"

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/chromosome="20"
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/gene="STAG1/PMEPA1"
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YGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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                                                                                                                                                                                                                                                                             Gaps
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/codon_start=1
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HS718J7

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where diliberances are found these are annocated as variations where diliberances are found these are annocated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGPChr20

This sequence is the entire insert of clone RP4-718J7 The true left end of clone RP4-579F0 is at 43945 in this sequence.

RP4-718J7 is from the library RPCI-4 constructed by the group of pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk requests: clone-trequest@sanger.ac.uk On Dec 5, 2000 this sequence version replaced gi:10198628. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
Human DNA sequence from clone RP4-718J7 on chromosome 20913.31-13.33 Contains the PCKI gene for soluble phosphoenolpyruvate carboxykinase 1, part of a novel gene similar to mouse DLM-1 (tumour stroma and activated macrophage protein), the 3' end of the TMEPAI gene encoding an androgen induced lb transmembrane protein (PMEPAI), two putative novel genes, a CpG island, ESTS, STSS and GSSS, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                              AL035541.15 GI:11546043
HTG; CpG island; DLM-1; macrophage protein; PCK1;
phosphoenolpyruvate carboxykinase; PMEPA1; TMEPA1; transmembrane
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/note="33 copies 53 mer 54% conserved"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/note="893 copies 2 mer
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/clone="RP4-718J7"
/clone_llb="RPCI-4"
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/note="5 c
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799. .3896
note="Charliel repeat: matches 681. .781 of consensus"
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3559. .13726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378. .3426 note="LIMB4 repeat: matches 6088. .6136 of consensus"
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hote="All repeat: matches 1. .34 of consensus"
1863. .921v
note="MLTID repeat: matches 105. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228. .9746
note="L2 repeat: matches 1459. .2028 of consensus"
880. .10089
note="L2 repeat: matches 2292. .2511 of consensus"
0094. .10206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .300 of consensus"
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1816. .12380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                952. .7021
note="L2_repeat: matches 2637. .2705 of consensus"
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2519. .12813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331. .5793
note="MLT1B repeat: matches 14. .466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  592. .6723
note="FLAM_C repeat: matches 1. .132 of consensus"
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note="AluSx repeat: matches 1. .312 of consensus"
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complement(13622. .14142)
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note="66 copies 2 mer tc 68% conserved"
3588. .13715
                                          note="4 copies 161 mer 64% conserved"
204. .1371
note="3 copies 56 mer 75% conserved"
                                                                                                                                                                                              675. 2718
note="18 copies 58 mer 55% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                      copies 55 mer 60% conserved"
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uote="4 copies 57 mer 86% conserved"
028. .2632
note="11 comies"
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228. .2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797. .5988
note="6 copies 32 mer 86% conserved"
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/note="3 copies 32 mer 79% conserved"
15021. .15110
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note="AluJb repeat: matches 188.
0263. .10573
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4313. .14437
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/note="4 ~
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note="2 cop
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note="28 cc
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// Acce="Will repeat: matches 86. .211 of consensus"
18312. .18438
// Acce="Will repeat: matches 138. .250 of consensus"
18585. .18776
// Acce="Will repeat: matches 7. .217 of consensus"
19211. .19290
// Acce="Will repeat: matches 72. .154 of consensus"
20413. .20463
// Acce="Will repeat: matches 90. .143 of consensus"
complement (21005. .21672)
// Acce="Mill repeat: matches 90. .143 of consensus"
// Acce="Mill repeat: matches 90. .143 of consensus"
// Acce="Mill repeat: matches 90. .143 of consensus"
// Acce="Mill repeat: matches 90. .143 of consensus"
// Acce="Match: 21052. Em:AQ748384"
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7603. .27684
note="L2 repeat: matches 2661. .2739 of consensus"
7823. .28041
                                                                                                                                                                                                                                              5273. .15399
Note="L2 repeat: matches 2159. .2285 of consensus"
5420. .15721
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hote="2 copies 35 mer 100% conserved"
4257 . 24591
note="L2 repeat: matches 2336 . 2710 of consensus"
1580 . 25611
note="16 copies 2 mer tc 87% conserved"
6333 . 26643
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6575. .16690
Motes"L2 repeat: matches 2596. .2711 of consensus"
8049. .19169
                                                                                                                                                                                                                                                                                                                                                     note="AluSx repeat: matches 1. .303 of consensus"
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'note="AluSx repeat: matches 1. .298 of consensus"
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1667. .21775
note="MIR_repeat: matches 73. .192 of consensus"
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                                                                                                                                    note="14 copies 6 mer cacaca 82% conserved"
5029. .15108
                                                                                                                                                                                                         note="20 copies 4 mer acac 83% conserved"
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Pred. No. 5e-131;
0; Mismatches 8; Indels
copies 2 mer ac 80% conserved"
                                                                                                                                                                                                                                                                                                                                                                                  6333. .16396
note="2 copies 32 mer 98% conserved"
                                 5026. .15109
note="7 copies 12 mer 82% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (21187. 21672)
/note="match: GSS: Em:AQ776209"
complement (21278. 21663)
/note="match: GSS: Em:AQ136459"
complement (21392. 21672)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Turi, T.G.
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/mol_type="genomic DNA"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                    TCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGG
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Cortact: MGC help desk
2.7e-111;
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Direct Submission
                683; Conservative
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Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin.B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,N.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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5.5e-100;
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Web site: http://www.nisc.nih.gov/
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Pred. No. 5.
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/mol_type="mRNA"
/strain="CZECH II"
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Best Local Similarity 78.5%;
Matches 776; Conservative (
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156698 bp DNA linear ROD 13-NOV-2002 sequence from clone RP23-4416 on chromosome 2, complete Mus musculus (house mouse) Mus musculus GI:25045360 49.4%; 81.9%; 876 861 TCCCCAGGGGGCCG Conservative gragadaccadadaca ALB37509 ALB37509.10 Similarity Mouse DNA sequence. AL837509 Local Simi hes 651; 202 274 502 295 622 682 742 802 862 94 142 331 382 442 502 562 622 682 82 322 386 442 847 Query Match 262 ACCESSION VERSION KEYWORDS SOURCE ORGANISM AL837509/c LOCUS DEFINITION Best Loca Matches RESULT ORIGIN 임 g Db g Dp g g g ઠે a ò 셤 ò 셤 ò g ò ద ò 셤 8 ò ò ò à ò ò õ /codon start=1
/proteIn\_id="CAD29011.1"
/broteIn\_id="CAD29011.1"
/db\_xref="G1:19700745"
/db\_xref="G1:19700745"
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1. 878
/organism="Mus musculus"
/mol type="genomic DNA"
/db xref="taxon:10090"
20. 844 1034 TAAGAGGCTTGCAAAAAAAAAAAA 1061 rcaaaaagcrrgcaaaaaagaaaaaa 1078 878 bp WO0216416. 247 g musculus (house mouse) musculus Sequence 12 from Patent AX392428 AX392428.1 GI:19700744 305 c AX392428 179 Mus 1 1051 562 622 648 682 708 742 802 862 914 933 974 991 RESULT 12
AX392428
LOCUS
DEFINITION
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561 141 153 201 213 261 273 321 330 381 385 441 441 501 501 561 621 621 681 681 741 CCCCACCTACAGGGAGGTCATTGGCCACTACCCTGGCTCCTTCCAGCACCAGCAAAG 741 801 801 861 802 GGA------GAACAAGGAGAAGGAGAAAAAGTCACCCCCTCTAGGA 846 AGGATGCCTCTGGCCCTCAGAGAGTACGGTGTCAGG---TGGAATGCCGGAGCCACAGGT ----AGCCGATTCCAACCCCTACCTCTACCTGCAGCACGAAATTGCCCTGCCACCAC CATCICACTGATGGGGAGGAGGGCCCCCACCTACCAGGGCCCCTGCACCCTCCAGCT TCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCCAAACAG ACGGACCCTGAGCAACAGCTGGAGCTGAACCGGGAATCTGTGCGCGCACCCCTAACCG GACCATCTTCGACAGTGACCTTATAGACAGCACCATGCTGGGGGGCCCCTGTCCCCCCAG CAGTAACTCGGGCATCAGCGCCCACGTGCTACGGCAGCGGCGCGCCATGGAGGGGCCCGCC GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAG AGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGATAAACAGAAAGGACACCCTCTAGGG 214 CCGCTCCTTCATCAGCCGACACAGCCAGGAGGAGAGAGACGATGGACTGTCCTCGGA CTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT TTTGTTCCCCAGCATGGAGATCACGGAGCTGGAGTTCGTGCAAATCGTGGTCATCGTGGT GGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAGCCCACTACAAGCTGTCTGC ACGCTCCTTCATCAGCCGGCACAGCGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGA <u> AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGT</u> CTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCAC CATCTCGCTGTCAGACGGGGAGGCCCCCACCCTACCAGGGCCCCTGCACCTCCAGCT Gaps 27; 878; Length Indels Score 523.8; DB 6; Pred. No. 1.2e-88; 0; Mismatches 117;

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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sww: SWISSPROT; Tr: TREMBL: WP: WORWPEP; Information on the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135162 CTGCACCTCCAGCTACGGACCCTGAGCAACAGCTGGAGCTGAACCGGGAATCTGTGCG 135103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135333 CCTCCAGCCACAGGTCTATGCCCCGCCTCGGCCCACTGACCGACTCGCTGTGCCCCCTT 135274
                                                                                                     Submitted (13-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 15, 2002 this sequence version replaced gi:24414713.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCG 546
  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-44L6 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 GGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                            During sequence assembly data is compared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.8%; Score 433.4; DB 10;
ilarity 77.3%; Pred. No. 9e-72;
Conservative 0; Mismatches 136; J
                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-23"
a 38596 c 39859 g 38800
                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
Chordata; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP23-44L6"
Eukaryota, Metazoa, Ch
Mammalia, Butheria, Ro
1 (bases 1 to 156698)
                                                                                     Direct Submission
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ORIGIN
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Dispublished

Signature, S., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Birren, B., Linton, L., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, Y., Cohangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, Y., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fizzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand, Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Marquis, N., Matthews, C., Micoa, T., McEwan, P., McKernan, K., Meldim, J., Mencus, L., Mihova, T., Merwan, P., McKernan, K., Maldim, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rostot, A., Santos, R., Schupback, R., Schupback, R., Schauer, S., Schupback, R., Seman, S., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Thacdore, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134698 -CAGGCTGAGTGGCCGTGTGGTAGTTCTCCTGTGTATAAATATTTACATGTTCTGT 134640
                                                                                                                                                        HTG 21-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              846
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 175754)
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Mus musculus clone RP23-41204, WORKING DRAFT SEQUENCE, 15 ordered
135102 CGCACCCCTAACCGGACCATCTTCGACAGTGACCTTATAGACAGCACCATGCTGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCACCAGCAGAGCAGTGGGCCCCCTCCTTGCTGGAGGGGACCCGGCTCCACCACAC
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                                                                                                                                                                                                                                                             CATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   847 ACACCCTCTCTAGGGTCCCCAGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAGGCAG--
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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**b-44.rge** 

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Direct Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Barra, N. Nusbaun, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Charga, J., Carlam, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacCand, P., MacCand, P., Major, J., Matchas, C., McCarthy, M., Mellim, J., MacCand, C., MacCand, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rise, C., Rogov, P., Roman, J., Roy, A., Schuer, S., Schuers, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talawas, J., Tesquer, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Li Submitted (11-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 21, 2002 this sequence eversion replaced gi:20455597.

All repeats were identified using RepeatMasker: html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Valel, R., Vo., Wilson, B., Wu, K., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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* Dy the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1773 8872: contig of 88772 bp in length

* 9560: contig of 688 bp in length

* 9660: gap of 100 bp

* 9661 10202: contig of 542 bp in length

* 10203 10302: gap of 100 bp

* 10303 11557: contig of 1455 bp in length

* 10303 11857: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 172000; agarose-fp
Insert size: 174354; sum-of-contrigs
Quality coverage: 11.2 in Q20 bases; agarose-fp
Quality coverage: 11.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L19642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1218 bp in length
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Web site: http://www-seq.wi.mit.edu
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                                                                                         TITLE
JOURNAL
                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                       AUTHORS
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146924 CCTCCAGCCACAGGTCTATGCCCCGCCTCGGCCCACTGACCGACTCGCTGTGCCCCCCTT 146983 307 CCCAGAGCCGCAGGTCTACGCCCCCGCCTCGGCCCACGACCGCCTGGCCGTGCCGCCTT 366 367 CGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGAT 426 38; Gaps Score 433.4; DB 2; Length 175754; Pred. No. 8.9e-72; 0; Mismatches 136; Indels 38; C contig of 16461 bp in length contig of 100 bp contig of 17161 bp in length contig of 23880 bp in length contig of 23880 bp in length contig of 31417 bp in length contig of 31417 bp in length gap of 100 bp contig of 53268 bp in length. of 3609 bp in length 100 bp 10f 6723 bp in length 100 bp 1412 others of 16461 bp in length 100 bp 100 bp of 3124 bp in length bp in length /organism="Mus musculus"
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/db\_xref="kraon:10090"
/db\_xref="krey23-41204"
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/clone="RPCI-23 Female Mouse BAC" 42511 a 44781 c 44000 g 43050 t 100 bp /note="assembly\_fragment" 9661. .10202 note="assembly\_fragment" 3176. .15093 note="assembly\_fragment" note="assembly\_fragment" 9412. .22535 note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note="assembly\_fragment" note≂"assembly\_fragment note="assembly\_fragment Location/Qualifiers contig gap of contig gap of gap of contig contig side:right" gap of clone\_end:SP6 \_\_\_ vector\_side:left" 22487. .175754 3168. .49628 5194. .19311 69806. .90869 2636. .26244 6345. .33067 9729. .66889 Query Match Best Local Similarity 77.3%; Matches 593; Conservative ( 122486: 668899 66699: 90869: 90969: 122386: 3873. 79560 26244: 49628: 49728: . . 8772 90970 122387 122487 66890 66990 22536 22636 26245 26345 33068 33168 49729 misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature source BASE COUNT ORIGIN FEATURES ò 셤 à

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                     147035 TGCCCTGCCACCCACCATCTCACTGTCTGATGGGGAGGAGCCCCCCACCCTACCAGGGCCC
                                                                           CTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCG
                                                                                                             147095 crecaccerceaecraceseaccercasceaecaecresascereaacceseaarcegeses
                                                                                                                                                     CGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGG
                                                                                                                                                                                                                                                                                                        667 CATGGAGGGCCGCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGGTCCTCTT
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ALB37520 176821 bp DNA linear HTG 01-JUN-2003
Mus musculus chromosome 2 clone RP23-41204, *** SEQUENCING IN
PROGRESS ***.
                                                      AL837520
AL837520.25 GI:31335607
                                                                                                                                                                              Direct Submission
                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL837520/c
                         DEFINITION
                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                            TITLE
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Submitted (199-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests. clonerequest@sanger.ac.uk Clon un 2, 2003 this sequence version replaced gi:3096480. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30. HTG; HTGS PHASE2; HTGS ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus ---- Genome Center COMMENT

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk Copract: humquery@sanger.ac.uk

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                            Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 176788 bases at least Q30
Consensus quality: 176819 bases at least Q30
Consensus quality: 176821 bases at least Q20
Insert size: 176821; sum-of-contigs
Insert size: 180785; 10.3% error; agarose-fp
Quality coverage: 9.74x in Q20 bases; sum-of-contigs Quality
coverage: 9.53x in Q20 bases; agarose-fp
                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 176821: contig of 176821 bp in length.

Location/Qualifiers
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28 444 29 444 29 30-44 31 43.8 33 43.8 33 43.8 33 43.8 33 43.8 33 63.8	09-252-91A-14 09-266-965-72 08-924-4401 08-924-4461 08-476-176B-5 08-476-176B-5 08-485-246A-9 09-194-905-68-3 09-252-991A-56 09-252-991A-56 09-252-991A-6	ALIGNMENTS  169482  SPECIFIC ANDROGEN-SIGNALING  1000  15/09/769,482  -26  179,722	Score 1022.4; DB 4; Len Pred. No. 3.1e-230; O; Mismatches 6; Inde AGGCTTGGGGGTTCGTGGCCATGA AGGCCTGGGGGTTCGTGGCCATGA FITTCCTGCGAAACCAGGCAATGGCGGAAGCAGGCAATGGCGGAAGCAGGCAATGGCGGAAGCAGGCAATGGCGGAAGCAGGCAATGGCGGAAGCAGCAATGGCGGAAGCAGCAATGGCGGAAGCAGCAATGGCGGAAGCAGCAATGGCGGGAAGCAGCAATGGCGGAAGCAATGGCGGAAGCAATGGCGGAAATGGCGGGAAGCAATGGCGGGAAGCAATGGCGGGAAGCAATGGCGGGAAGCAATGGCGGGAATGCCGGGAATGGCGGGAATGCCGGGAATGGCGGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGGGAAATGGCGGGAATGCCGGAATGCCGGGAATGCCGGGAATGCCGGAATGCCGGGAATGCCGGGAATGCCGGAATGCCGGGAATGCCGGAATGCCGGAATGCCGGGAATGCCGGAATGCCGGGAATGCCGGAATGCCGGGAATGCCGCGAATGCCGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGCGAATGCCGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGGGAATGCCGCGAATGCCGCGAATGCCGCGAATGCCGCGAATGCCGCGAATGCCGCGAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCAATGCCCGCAATGCCCGCAATGCCCCAATGCCCCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCGCAATGCCCCAATGCCCGCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCCAATGCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCAATGCCCCAATGCCCAATGCCCAATGCCCAATGCCCCAATGCCCCAATGCCCCAATGCCCAATGCCCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCAATGCCCAATGCCCAATGCCAATGCCCAATGCCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCAATGCCAATGCCAATGCAATGCCAATGCAATGCCAATGCCAATGCCAATGCCAATGCAATGCCAATGCAATGCAATGCCAATGCCAATGCAATGCCAATGCCAATGC
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US-09-769-482-2
is Sequence 2, Application US/09769482
is Sequence 2, Application US/09769482
is Sequence 2, Application US/09769482
is GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REPERENCE: 04995.0057-00000
CURRENT FILING DATE: 2001-01-26
CURRENT PILING DATE: 2001-01-26
PRIOR PPLICATION NUMBER: 60/178,772
PRIOR PPLICATION NUMBER: 60/178,772
PRIOR PPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/178,772
                                               GATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCCTACCAGGG
                                                                                                                                        GATCGACCTGCCACCCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCTACCAGGG
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                                                                                                                                           Length 759;
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                                                                                                                                           Score 757.4; DB 4;
Pred. No. 2.7e-168;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Detera-Wadleigh, S
Gershon, Elliot S.
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 759
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                           71.48;
99.98;
                                                                                                                                                           Best Local Similarity 99.9
Matches 758; Conservative
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US-09-091-952A-7
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US-09-769-482-2
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Pred. No. 9.7e-73;
0; Mismatches 160; Indels
                                                                                          Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPELICATION DAMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-COT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-COT-1997
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, TIMOCHY L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone 22 coding region SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                      COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
EBNGTH: 921 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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OTHER INFORMATION:
                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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Best Local Similarity 73.7
Matches 474; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-091-952A-7
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464 535 524 595 584 655 641 656 radacarriccrargraraccococorcearoceaeceaecaecaecaecreoceaecres CCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCA 701 716 caagcaccrecadcadraaccecaarecarecececececececeraracaeceaerea 775 465 AGCCCCACCCTACCAGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG ATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGG 536 AGCCACCTCCTTACCAGGGCCCTGCACCCTGCAGCTCCGGGACCCTGAACAGCAGGTGG AACTGAACCGGGAGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 596 AACTCAACCGAGAGTCCGTGAGGGCCCCACCCAACCGAACCATTTGACAGTGATTTAA Esterling, Lisa E. TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness TGGGCCACCAGGCGCCTTTTCCTCCATCACCAGGGCGCAG 818 TCGGCCACTACCCGGGGTCCTTCCAGCACCAGCAGCAG 744 STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUER: Diskette
MEDIUER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0 NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/OCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-99
CLASSIFICATION: Unknown>
PRIOR APPLICATION: Unknown>
PRIOR APPLICATION: UNBER: US 60/029,278
FILING DATE: 28-0CT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-0CT-1997
ATTORNET/AGENT INFORMATION: Sevilla D. APPLICANT: Detera-Wadleigh, Sevi Gershon, Elliot S. Badner, Judith A. Goldin, Lynn R. Bertettini, Wade H. Yoshikawa, Take Sequence 6, Application US/09091952A Patent No. 6458532 GENERAL INFORMATION: NUMBER OF SEQUENCES: 197 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and TELEFAX: (415) 5 TELEX: <Unknown> US-09-091-952A-6 416 525 642 702 176 405 585 ò 셤 ò g ð 셤 ò 셤 ò g ò 유

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 Accecrárgraciadades de articar circi de contracio de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contraciones de contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711 AACTCAACCGAGAGTCCGTGAGGGCCCCACCCAACCGAACCATATTTGACAGTGATTAA 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 ACAGGTTCACAGCGCCGTCCTTCATCCAGAGGGATCGCTTCAGCCGCTTCCAGCCCACCT
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OTHER INFORMATION: alternatively spliced portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 349; DB 4; Length 80 Pred. No. 1.9e-72; 0; Mismatches 160; Indels
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OTHER INFORMATION: Clone 22 coding region
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                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1...8065
OTHER INFORMATION: Clone 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEY: misc_feature
ION: 5595...5685
INFORMATION: ampl
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.9%;
Best Local Similarity 73.7%;
Matches 474; Conservative
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                                                                                                                                                                                                                                            TITLE OF INVENTION: Chromosomal Markers and Diagnostic TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Elghth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 015280-297100US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/029,278
PILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35.367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DĀTA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <UNknown>
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                                                                                                                                                       Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
                   Sequence 8, Application US/09091952A Patent No. 6458532 GENERAL INFORMATION:
                                                                                      APPLICANT: Detera-Wadleigh, S
Gershon, Elliot S.
Badner, Judith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 576-0300
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                           Sanders, Alan R
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                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1...867
OTHER INFORMATION:
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Best Local Similarity
US-09-091-952A-8
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Sequence 13650, Application US/09252991A

Sequence 13650, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15550
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Patent No. 5352596

GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The EPO and LLT Genes
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
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STREET: 1815 No. 5352596th University Street
CITY: Peoria
607 TCGCGGAGGCGGATAGCCGCCCTGGC 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.8°
Matches 85; Conservative
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US-07-945-283-1/c
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STATE: II
COUNTRY:
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Sequence 13687, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
APPLICATION:
AUCHIEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-17

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 13687

LENGTH: 696
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                       GCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
                                                                                                                      285 GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCCGCCTCGGCCCACCG
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4.5%; Score 47.8; DB 4; Length 696;
Best Local Similarity 57.8%; Pred. No. 0.025;
Matches 85; Conservative 0; Mismatches 62; Indels
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                                                                    302 ACCAGAGCCGGAGGCGGAGGACGGCT----
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US-09-252-991A-13687
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US-09-252-991A-13687
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Pred. No. 0.054;
309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudorabies virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variation
replace(7010, "g")
                             TELEFAX: 309-685-4128
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.4%;
Matches 189; Conservative
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622..6495
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ORIGINAL SOURCE:
ORGANISM: PSE
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FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
US-07-945-283-1
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FEATURE:
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Sequence 42, Application US/09266965 Patent No. 6495348 GENERAL INFORMATION:

US-09-266-965-42/c

APPLICANT: Sherman,

APPLICANT

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Pred. No. 0.037;
0; Mismatches 196; Indels 1
APPLICANT: Bheldon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster:
FILE REFERENCE: 600.456USI
FILE REFERENCE: 600.456USI
CURRENT PAPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER PILING DATE: 1999-08-19
EARLIER PILING DATE: 1994-10-06
EARLIER PILING DATE: 1994-10-06
EARLIER PILING DATE: 1994-10-07
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER PILING DATE: 1993-10-07
SARIER PILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 1215
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APPLICANT: Mao, Y
APPLICANT: Waroglu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TILLE OF INVENTION, MICHORYCIN blosynthetic gene cluster
FILE REFERENCE: 600.456031
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1996-03-12
EARLIER PILING DATE: 1996-08-19
EARLIER FILING DATE: 1996-08-19
EARLIER FILING DATE: 1994-10-06
EARLIER FILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: US 08/133,963
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Patent No. 6495348
GENERAL INFORMATION:
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; ORGANISM: Streptomyces lavendulae.
US-09-266-965-42
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Best Local Similarity 47.24
Matches 176; Conservative
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NS-09-152-991A-4200/c

i Sequence 4200, Application US/09252991A

petcert No. 6551795

i GRNERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

I TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

I TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PELING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 4200

LENGTH: 1611
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
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                                                                                                                              CCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAG 591
                                                                                                                                                                                                          295 GCCGGTGCGCCTGCACGTATCGGCCCAAGCGCTTCCTCTGCGCGGGGGACCCGAGCTACCA 354
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Pred. No. 0.071;
0; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4391
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Best Local Similarity 51.2%;
Matches 108; Conservative (
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US-09-252-991A-4586

Squence 4586, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
PAPLICANTON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 561
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4.5%; Score 47.4; DB 4; 1
Best Local Similarity 47.2%; Pred. No. 0.12;
Matches 176; Conservative 0; Mismatches 196;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 76
LENGTH: 53500
                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-76
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US-09-252-991A-4586
EARLIER FILING DATE: 1993-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13876 receeececec 13888
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                                                                                                                                                                                                                              472 ACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAA
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                                                                              DB 4; Length 1611;
                                                                          Score 46.2; DB 4; Length 1 Pred. No. 0.078; 0; Mismatches 103; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: PROFICE IN STATEMENT APPLICATION NUMBER: US/08/785,420
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 08/249,388
FILING DATE:
APPLICATION NUMBER: US 08/030,159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08785420
Patent No. 6001976
GENERAL INFORMATION:
APPLICANT: AMACLEDIAN, David H
APPLICANT: O'Brien, Peter J.
TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
TITLE OF INVENTION: HYPERTHERMIA
                                                                                                                                                                                                                                                                                                                                                                                                                1294 cécchéccrérceccescricceschade 1264
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CORRESPONDENCE ADDRESS:
ADDRESSE: Bell, Seltzer, Park & Gibson STREET: P.O. Drawer 34009
CITY: Charlotte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 6001976th Carolina 28234 : U.S.A.
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ATTORNEY/AGENT INFORMATION:
NAME: LAYLON, Jr., Samuel G
REGISTRATION NUMBER: 22807
REFRENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561
; TYPE: DNA
; ORGANISM: Pgeudomonas aeruginosa
US-09-252-991A-4200
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 15378 base pairs TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE. NO
                                                                        Query Match
Best Local Similarity 51.2%;
Matches 108; Conservative
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US-08-785-420-1/c
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STATE: No
COUNTRY:
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US-09-252-991A-692
Sequence 692, Application US/09252991A
Sequence 692, Application US/09252991A
Sequence 692, Application US/09252991A
Sequence No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PELICATION NUMBER: US/09/252,991A
FRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13269 GGGCATGCCCGCCAGGAGCTCGGTCACCGTCACCTTGTTGGCACCCTCCACCAGGCCGCC 13210
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                                                                                                                                                                                                                                                                                                                                                                                                                               380 GGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCC
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                                                                                                                                                                               Query Match
4.4%; Score 46.2; DB 3; Length 1.
Best Local Similarity 50.7%; Pred. No. 0.15;
Matches 111; Conservative 0; Mismatches 108; Indels
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Pred. No. 0.11;
0; Mismatches 170; Indels
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US-09-252-991A-692
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IMMEDIATE SOURCE:
CLONE: Porcine RYR1 Gene
POSITION IN GENOME:
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Best Local Similarity 46.5
Matches 148; Conservative
                                                                                             UNITS: bp
                                                                                                                             US-08-785-420-1
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17:50:12 2003 Tue Dec

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Search completed: December 8, 2003, 03:57:31 Job time : 84 secs

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Ltd.		h time 2637 Seconds alignments) Million cell updates/sec	.cttgcaaaaaaaaaaaaa 1061			45562784			y chance to have a e result being printed, distribution.	ion	AL517150 AL517150 AL578575 AL578575 AL558882 AL558882 AL558881 AL558881
GenCore version 5.1.6 (c) 1993 - 2003 Compugen	ng sw model	01:15:30 ; Searc (without 9778.934	4 gggtga	ext 1.0	12152238056 residues	chosen parameters:	0	0% 1100% 45 summaries	results predicted b to the score of th of the total score SUMMARIES	ID	AL517150 AL578575 AL558882 AL558881
	, using	, 2003,	-826B-4 tgggttc	c , Gapext	ведв, 1		2000000000	Match 0 Match 1 first 4		Δ :	10 <i>C</i> 1
Copyright	search,	er 8	857-8 ccttg	TY_NU 10.0	92	satisfying	2000	num Ma num Ma ng fi	TI:  em_esthum:* em_estin:* em_estou:* em_estou:* em_esto:* em_esto:* em_esto:* gb_est:* gb_est:* gb_est:* gb_ests:* em_gss_hum:*	Lengt	1201 1009 1007 951
Cop	nucleic E	December	US-09-857- 1061 1 tcctcctt	IDENTITY_NUC Gapop 10.0 ,	227813	hits s	length: length:	Minimum Maximum Listing	EST:*  1: EST:*  2: eman and and and and and and and and and a	Match Length	83.8 82.8 80.9 79.6
	•		score:	table:	ä	number of	DB seq 1 DB seq 1	Post-processing:	ed	Score	889.4 878.4 858.8 844.2
	OM nucleic	Run on:	Title: Perfect Sequence	Scoring	Searched	Total nu	Minimum Maximum	Post-pro	Database Pr BG an Result	No.	00 0 

5         74.4         74.9         874         13 BX362396           7         773         72.9         874         13 BX362396           7         773         72.9         967         13 BQ641849           8         768.4         72.4         782         12 BQ671810           9         724.4         78.2         13 BQ641849           10         720.2         67.9         729         13 BQ641110           11         709.8         66.9         728         13 BQ680150           12         697.8         66.9         728         13 BQ680150           13         66.9         66.9         728         13 BQ6801750           14         652.         61.5         655         13 BQ6801750           15         66.9         728         13 BQ6801750           16         66.9         728         13 BQ6801760           17         636.2         61.3         14 BQ680170           18         61.2         60.0         64.0         13 BQ680170           19         60.0         64.0         13 BQ680170           20         60.0         64.0         13 BQ680170           21 <td< th=""><th></th><th>_</th><th></th><th>BM677602 UI-E-EO1-</th><th></th><th></th><th>BQ690750 AGENCOURT</th><th></th><th>AI761441 wg65f07.x</th><th></th><th>_</th><th>BU730650 UI-E-CII-</th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th>BU157959 AGENCOURT</th><th>56 A</th><th>3</th><th></th><th>BQ575582 UI-H-EZ1-</th><th>BQ954555 AGENCOURT</th><th>A1972096 wr62d11.x</th><th>BE855409 /GISIUS.X</th><th>AI742327 wg50£07.x</th><th>BM141979 1125all.y</th><th>BM676516 UI-E-EJO-</th><th>BM713900 UI-E-EJO-</th><th>OO NISC</th><th>1 tc37c07</th><th>908976</th><th>wk42g04</th><th>85001 w188c11</th></td<>		_		BM677602 UI-E-EO1-			BQ690750 AGENCOURT		AI761441 wg65f07.x		_	BU730650 UI-E-CII-											BU157959 AGENCOURT	56 A	3		BQ575582 UI-H-EZ1-	BQ954555 AGENCOURT	A1972096 wr62d11.x	BE855409 /GISIUS.X	AI742327 wg50£07.x	BM141979 1125all.y	BM676516 UI-E-EJO-	BM713900 UI-E-EJO-	OO NISC	1 tc37c07	908976	wk42g04	85001 w188c11
794.4 74.9 874 77.7 77.6 73.1 9875 77.7 77.6 73.1 9875 77.7 77.6 73.1 9875 77.7 77.6 73.1 9875 77.7 77.7 77.1 9875 77.7 77.7 77.1 9875 77.7 77.7 77.1 9875 77.7 9875 7	BX36239 BU53921 BQ64184	BQ01517							~																AW071693	BU15784	BQ57558	BQ95455	A1972096	BERDD40	AI742327	BM14197	BM67651	BM71390	CB04980	8	ĭ	_	$\overline{}$
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	77	768.4	724.4	720.2	709.8	697.8	680.2	652	644.2	636.2	635.2	612.4	609.2	609	605	599	594.8	592.8	591	587.2	585	578	578	573	572.2	569.4	562.2	562.2	258.2	000	555.8	548.4	534	534	534	528.6	523.8	515.8	502
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## ALIGNMENTS

AL517150 1201 bp mRNA linear EST 09-MAY-2003 AL517150 Homo sapiens NEUROBLASTOWA Homo sapiens cDNA clone CS0DA008YB23 3-PRIME, mRNA sequence. AL517150.2 GI:30492472 EST. ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT.1 AL517150/c LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT

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// organism="Homo sapiens"
// organism="mRNA"
// or
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llarity 97.2%; Pred. No. 6.3e-157;
Conservative 1; Mismatches 24;
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http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
Location/Qualifiers
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ALS78575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens cDNA clone CSODK001YC24 3-PRIME, mRNA sequence.
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
293 c 344 g 201 t 11 others
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Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Livitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODK001BB12NP1&cluster=9945.r. Contact :
Feng Liang Email: fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK001BB12NP1.
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                     160 TCCCCAGGGGGGCCGGGCTGGGGCTGAAAAGGCAGAACACTCCGCGCTTCTT
                                                                           AGAAGAGGAGTGAGAAGGCGGGGGGGCGCAACGCATCGTGTGGCCCTCCCCTCCC
                                                                                                Gaps
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Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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Mammalia, Eutheria, Primates, Catarrhini, Hon
1 (bases 1 to 1009)
Li/W.B., Gruber, C., Jessee, J. and Polayes, D.
Wull-length cDNA libraries and normalization
Unpublished
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Pred. No. 7.5e-155;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK001YC24"
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96.3%;
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
On Peb 15, 2001 this sequence version replaced gi:12903838, Contact: Genoscope
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/clone lib="Homo sapiens T_CELLS (J 10-NORWALIZED")
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E Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

E Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2011 this sequence version replaced gi:12903836.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 131 91006 EVRY codex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

9945.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODJ015DC06ND1&cluster=9945.r. Contact:

Feng Liang Email: fliangelifetech.com URL:

Franday Avenue Genoscope sequence ID: CSODJ015DC06NP1.
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10-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
275 c 318 g 201 t 16 others
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Pred. No. 1.9e-148;
2; Mismatches 6;
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874 bp mRNA linear EST 05-MAY-2003 HA362396 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CS0DJ014YN15 3-PRIME, mRNA sequence. BX362396. I GI:30378625
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Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
Email: seqref@genoscope.cns.fr /
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODJ014CGOBNP1&cluster=9945.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODJO14CGOBNP1.
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/cell tine="JURKAT"
/cell tib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the prime vector. Library was normalized."
257 c 278 g 180 t 34 others
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al Similarity 94.3%; Score 794.4; DB 13; Length
al Similarity 94.3%; Pred. No. 4.3e-139;
824; Conservative 20; Mismatches 27; Indels
                                 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                               Unpublished
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/tissue type="adencarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NNH MGC 107"
/clone lib="NNH MGC 107"
/note="Organ: breast, Vector: pOTB7; Site_1: EcoRI;
Site_2: KhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH—MGC Library."
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                                                                                                                                                            TGGGCCGCCCTCCTTGCTGGAGGGACCCGCCTCCACCAMACACACATCGCGCCCCTAGA
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Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
plate: LLCM2757 row: p column: 18
High quality sequence stop: 663.
Location/Qualifiers
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bussy219
AGENCOURT 10215265 NIH_MGC_107 Homo sapiens cDNA clone IMAGE5659922 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 967)

NHH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2493 row: g column: 18
High quality sequence stop: 571.

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Note: this is a NIH MGC Library. | "
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DEFINITION RESULT 7 BQ641849

bp mRNA linear EST 15-JUL-2002 Homo sapiens cDNA clone IMAGE:6292265 BQ641849 AGENCOURT\_8287174 NIH\_MGC\_43 HC 5', mRNA sequence. BQ641849 BQ641849.1 GI:21766021 EST ACCESSION VERSION KEYWORDS

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782 bp mRNA linear EST 26-MAR-2002 IN-H-ED1-axw-k-20-0UI.81 NCI CGAP_ED1 Homo sapiens cDNA clone RQO15170 BQ015170 IN-19740071
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Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA=Yes.
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1 (Dases 1 to 782)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Umpublished
                                                                                                                                      GATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACG
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'db_xref="taxon:9606"
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Seg primer: M13 FORWARD
POLYA-Yes.
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                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 729)

                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
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Pred. No. 5.8e-126;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 725; Conservative
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Homo sapiens
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ORIGIN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                             549 AGCAGCTGGAACTGAACCGGGAGTGCGCGCGCACCCCCAAACAGAACCATCTTCGACA
                                                                                                                                                                                                                                                                                                                                                                      309 CCTTGCTGGAGGGGACCCGGCTCCACCACACACACGCGCCCCTAGAGAGGCGCACA
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609 ACGGGGAGGACCCCCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              696 AGGTCATTCGGCCACTACCCGGGGTCCTTCCAGCACCAGCAGCAGCAGTGGGCCCCT
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                                                                                                                                                                                                                                                                                                                     BM677602
UI-E-EO1-aid-p-09-0-UI.sl UI-E-EO1 Homo sapiens CDNA clone
UI-E-EO1-aid-p-09-0-UI 3', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/clone_lib="UI-E-EO1"
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99.3%; Pred. No. 3.5e-125;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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/tissue_type="fetal eye"
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University of Iowa
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Seq primer: M13 FORWARD
POLYA-Yes.
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="U11-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU683523 70-0CT-2002
UI-CF-EC1-acg-e-09-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-acg-e-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                               995 TAAATATTTACATGTGATGTCTGGATGCACAAGCTAAGAGAGCTTGCAAAAAAA 1054
                                                                                                 934
                                                                                                                                             190 cececrececreceraceraaaaececaaacacrecececrrerragaagacaerea 131
                                                                                                                                                                                             994
                                                250 ATCTGGAGCAAAGAQAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGC 191
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                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 728)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                         130 GAGGAGGGGGGGGCGCAGCAACGCATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTA
                                                                                              875 CGGGCTGGGGCTGCGTAGGTGAAAGGCAGAACACTCCGCGCTTCTTAGAAGAGGAGTGA
                                                                                                                                                                                             935 GAGGAAGGCGGGGGCGCAACGCATCGTGTGGCCCTCCCCTCCCACCTCCCTGTGTA
  ATCTGGAGCAAAGAAGGATAAACAGAAAGGACACCCTC1
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/db xxef="taxon:9606"
/clone="Ul-CP-EC1-acg-e-09-0-Ul"
/tissue_type="Lung"
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/organism="Homo sapiens"
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      Synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pyTT3-Pac vector. The oligomacleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG ILB-UI-CF-ECI
TAG TISSUE-Normal Lung Epithelial Cells Tissue nos 369-371 and 389-383
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Research, 6:791-806,
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llarity 99.4%;
Conservative 0
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/done lib="Mild (11-phage resistant)"
/done lib="Mild (11-phage resistant)"
/done="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccactcaggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line poly4+ RNAs (bladder-2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon-4%, connective tissue - 1.4%, eye - 1%, incestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AATCTAGAGGCCAGGCGCACATG-GT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SNART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH MGC 141).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH MGC Library."
        950 bp mRNA linear EST 20-SEP-2002 1016502 NIH MGC 142 Homo sapiens cDNA clone 853 5', mRNA sequence.
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                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 850)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov i column: 22
High quality sequence stop: 499.
Location/Qualifiers
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Pred. No. 5.4e-121;
); Mismatches 52; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:6497853"
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/lab_host="DH10B (Tl-phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                   BU602918.1 GI:23254677
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92.9%;
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IMAGE:6497853 5'
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TITLE
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**b-44**.rst

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/mol_type="mRNA"

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High quality sequence stop: 627
Location/Qualifiers
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1 (bases 1 to 890)
1 MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llh.gov
Plate: LLCM2368 row: h column: 14
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5', mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /done="IMAGE:62089"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="UHH MGC_ll0"
/note="Organ: pancreas; Vector: poTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGACGGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
                                                                                                                                               BQ691705

AGENCOURT 8046876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208939

$\text{S}', mRNA sequence.}

BQ691705
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
High quality sequence stop: 645.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCAGCGGCGGCGCATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCAC 709
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 CCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 TACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGGAGCCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
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/db xref="taxon:9606"
737
                                       744 GGGTCCCTCCTTTCCAGC 762
                                                                                                                                                                                                                 BQ691705.1 GI:21817021
EST.
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TITLE
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KEYWORDS
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/clone_lib="Soares NSF F8 9W OT PA P S1"
/note="Organ: pooled; Vector: pT713D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
pCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneDEs: Soares NBAFF pool 1:
309384-310919, 323208-325895 Soares NBZHP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NbZHF9-9W pool 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI761441 693 bp mRNA linear EST 20-DEC-1999 wg65£07.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens CDNA clone IMAGE:2369989 3' similar to TR:015168 CLONE 22. [3] TR:015167 TR:015165 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1009
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1 (bases 1 to 693)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Confact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1105 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 464.
                                                                                                                                                                    301 TACCCGGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGGAGGGG
                                                                                                                                                                                                                                                                                                 361 Accedecticaceacacacacacacecececeracacacececateresassas
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/organism="Homo sapiens"

/mol type="mRNN"

/db_xref="taxon:9606"

/clone="TMAGE:236989"

/lab_host="DH108"
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758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322833, 326280-32663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Benl
Soares and M. Fatima Bonaldo." 1 others
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                                                                                                                Query Match 60.7%; Score 644.2; DB 9; Best Local Similarity 98.1%; Pred. No. 6.2e-111; Matches 683; Conservative 0; Mismatches 9;
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Search completed: December 8, 2003, 03:56:09 Job time : 2647 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model Run on:

December 8, 2003, 01:56:10 ; Search time 1262 Seconds (without alignments) 2794.246 Million cell updates/sec

US-09-857-826B-44 Title:

Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

2201672 seqs, 1661799599 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

4403344

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

(cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

(cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

(cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de				
Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description
4	1034.4	97.5		13	US-10-301-822-208	Sequence 208, App
7	1034.4	97.5		15	US-10-205-823-412	Sequence 412, App
m	1034.4	97.5		13	US-10-241-220-44	44. A
4	1034.4	97.5	4527	13	US-09-821-812-2	Sequence 2, Appli
S	1022.4	96.4		13	US-10-390-045-1	H
ø	1021.2	96.2		14	US-10-098-841-71	Sequence 71, Appl
7	961.8	90.7		11	US-09-796-753-55	
80	926	90.1		13	US-10-241-220-119	Sequence 119, App
σ	926	90.1	Ī	13	US-10-269-909-84	Sequence 84, Appl
10	926	90.1		13	US-10-269-909-85	Sequence 85, Appl
11	800.6	75.5		10	US-09-934-249-1	Sequence 1, Appli
12	795.2	74.9		13	US-10-241-220-45	Sequence 45, Appl
13	757.4	71.4		13	US-10-390-045-2	Sequence 2, Appli
14	752.6	70.9		10	US-09-934-249-3	Sequence 3, Appli
15	728.8	68.7		15	US-10-000-256A-32	Segmence 32. Appl

Sequence 14, Appl Sequence 12, Appl Sequence 17, Appl Sequence 197, Appl Sequence 16, Appl Sequence 0, Appli Sequence 0, Appli Sequence 15, Appl Sequence 1481, Appl Sequence 1483, Appl Sequence 1481, Appl Sequence 1416, Appli Sequence 1416, Appli Sequence 1, Appli	22 4 4 5 7 6 7 7 6 7 7 6 7 7 6 7 7 6 7 7 6 7 7 6 7 7 6 7 7 6 7 7 7 6 7
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## ALIGNMENTS

APPLICANT: Milennium Frarimaceulicais, Auc.
APPLICANT: Berger: Allieon
APPLICANT: Berger: Allieon
APPLICANT: Schlegal, Robert
APPLICANT: Schlegal, Robert
APPLICANT: Schlegal, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: NUNEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: WETHODS FOR IDENTIFICATION NUMBER: US 60/339, 971
PRIOR APPLICATION NUMBER: US 60/361, 978
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361, 978
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 208
TENCRELL ABSECT OF Windows Version 4.0
SSEQ ID NO 208 APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L. Sequence 208, Application US/10301822 Publication No. US20030148410A1 TYPE: DNA ORGANISM: Homo Sapiens ; NAME/KEY: CDS ; LOCATION: (96)...(854) US-10-301-822-208

97.5%; Score 1034.4; DB 13; Length 1141; 99.2%; Pred. No. 8.6e-274; Query Match Best Local Similarity

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APPLICANT: Gannavarapu, Manjula
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APPLICANT: Kamatkar, Shubhangi
APPLICANT: Galtt, Karen
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRICE REPRENCE: 2002-07-25
FILE REPERBURE: MRI-047-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR PELING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR PILING DATE: 2001-09-25
PRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-109-25
PRIOR PELING DATE: 2001-12-12
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Pred. No. 8.6e-274;
0; Mismatches 6; I
5-10-205-823-412
Sequence 412, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
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                                                                                                                                      APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
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Best Local Similarity 99.2
Matches 1050; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412
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Matches 1050;

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GGGGGACCCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGG

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CTTCCAGCACCAGCAGAGCAGTGGGCCCCCTCCTTGCTGGAGGGGACCCGGCTCCACCA CACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGGAGCAAAGAGAAGGATAAACAGAA CACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGAGATAAACAGAA 719 784 779 Dp 셤 ò

778 843 838 903 898 963

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FOR THE DIAGNOSIS

Sequence 44, Application US/10241220

Publication No. US20030148408A1

GENERAL INFORMATION:

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Phillipp, Heaid

APPLICANT: Phillipp, Paul

APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

APPLICANT: Any Thomas

APPLICANT: Cannow TREATMENT OF TUMOR

TITLE OF INVENTION: COMBER: US/10/241,220

CURRENT PILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 120

GTGTGGCCCTCCCTCCCTCCCTGTGTATAAATATTTACATGTGATGTCTGGA GIGHTON CONTROLL CONTROL 64 959 g g ò

ATGCACAAGCTAAGAGGCTTGCAAAAAAAAAAAA 1061 1024

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Score 1034.4; DB 13; Length 1850; Pred. No. 9.7e-274;

97.5%;

Query Match Best Local Similarity

TYPE: DNA ORGANISM: Homo SEQ ID NO 44 LENGTH: 1850

US-10-241-220-44

1018

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NAME/KEY: CDS
LOCATION: (95
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                                                                                            Specific
                                                                                            Prostate
                                 Sequence 2, Application US/09821812
Publication No. US20030166520A1
GENERAL INFORMATION:
APPLICANT: Lin, Biaoyang
TITLE OF INVENTION: Androgen Regulated Prost:
TITLE OF INVENTION: Andrejc Acids
FILE REFERENCE: P.IS 437
CURRENT APPLICATION NUMBER: US/09/821,812
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: ESECENCE OF Windows Version 4.0
                                                                                                                                                                                                LENGTH: 4527
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (96)...(851)
US-09-821-812-2
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; Sequence 1, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: EAGAWA, TRACKHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; TITLE OF INVENTION: POYNUCLEOTIDE
; PRIOR APPLICATION NUMBER: US/10/390,045
; PRIOR PILING DATE: 2001-01-28
; PRIOR APPLICATION NUMBER: 60/178,72
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR PILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-28
; PRIOR PILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-28
719 CTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCTCCACCA
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Pred. No. 1.7e-270;
0; Mismatches 6; Indels 3;
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SEQ ID NO 1
LENGTH: 1140
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Matches 1049; Conservative
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APPLICANT: Ma, Yunqing
APPLICANT: Wang, Jian-Rui
APPLICANT: Raho, Qing A.
APPLICANT: Raho, Qing A.
APPLICANT: Raho, Qing A.
APPLICANT: Raho, Qing A.
APPLICANT: Raho, Rui-hong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Jiane
APPLICANT: Dramang, No. US20020197679Alel Nucleic Acids and
TITLE OF INVENTION: No. US20020197679Alel
TITLE OF INVENTION: No. US20020197679Alel
TITLE OF INVENTION: NO. US20020197679Alel
TITLE OF INVENTION: NOWBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR PILING DATE: 2000-04-25
PRIOR PELICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: PL_Genes Version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (154)..(867)
US-10-098-841-71
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      GATCATCATCATCGTGGTGGTGATGGTGATGGTGGTGGTGATCACGTGCTGCTGCTGAG 177
                                                                                                   244 AGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGG
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 Score 1021.2; DB 14; Length 1066;
Pred. No. 3.6e-270;
0; Mismatches 8; Indels 7;
Query Match
Best Local Similarity 98.6%;
Matches 1043; Conservative
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Sequence 71, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping

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                                                                         609 GGGCGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACAGGCAGCGG
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  549 GGTGCGCGCACCCCCAAACAAACATCTTCGACAGTGACCTGATGGATAGTGCCAGGCT
                                                 601 GGGCGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGG
                                                                                                                                          661 CGGCCCATGGAGGGCCGCCCCCCCTACAGCGAGGTCATCGGCCACTACCCGGGGTC
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; Bequence 55, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
    APPLICANT: MCCARTHY, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: 08/09/796,753
; CURRENT PILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR PILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR PLING DATE: 1998-12-30
; PRIOR PLING DATE: 1999-02-26
; PRIOR PLING DATE: 1999-02-26
; PRIOR PLING DATE: 1999-02-26
; PRIOR PLING DATE: 1999-06-14
; PRIOR PLING DATE: 1999-06-14
; PRIOR PLING DATE: 1999-06-14
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Pred. No. 6.9e-254;
0; Mismatches 2; Indels 0;
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-29
PRIOR PLING DATE: 1999-12-29
PRIOR PRIOR APPLICATION NUMBER: 09/514,010
PRIOR PLING DATE: 2000-02-5
PRIOR PRIOR DATE: 2000-03-01
PRIOR PLING DATE: 2000-05-01
PRIOR PRIOR DATE: 2000-05-19
PRIOR PRIOR DATE: 2000-05-19
PRIOR PRIOR DATE: 2000-05-19
PRIOR PRIOR DATE: 2000-05-19
PRIOR PRIOR DATE: 2000-05-19
PRIOR PLING DATE: 2000-06-29
PRIOR PRIOR APPLICATION NUMBER: 09/599,596
PRIOR PRIOR APPLICATION NUMBER: 09/606,317
PRIOR APPLICATION NUMBER: 09/606,317
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; LOCATION: (6)
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Pred. No. 4e-252;
0; Mismatches 15; Indels 0
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Best Local Similarity 98.5%;
Matches 965; Conservative
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; ORGANISM: Homo Sapien
US-10-241-220-119
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US-10-269-909-84
IS-QUENCE 84, Application US/10269909
| Sequence 84, Application US/10269909
| Publication No. US20030180747A1
| GENERAL INFORMATION:
| APPLICANT: HRUBAN, RALPH H.
| APPLICANT: HRCBAN, PEDRAM
| APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
| APPLICANT: MAITRA, ANIRBAN
| TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
| FILE REFERENCE: SA303(71699)
| CURRENT APPLICATION NUMBER: US/10/269,909 1042 CTTGCAAAAAAAAAAAAA 1061

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0
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                                                                                                                                                                                              Indels
                                                                                                                                                                                               15;
                                                                                                                                                                       DB 13;
                                                                                                                                                                     Query Match 90.1%; Score 956; DB 13
Best Local Similarity 98.5%; Pred. No. 4e-252;
Matches 965; Conservative 0; Mismatches 1
CURRENT FILING DATE: 2003-10-11
PRIOR APPLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/332,754
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 84
LENGTH: 4839
                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-269-909-84
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APPLICANT: HUNCANALION:

APPLICANT: ARGANI, PEDRAM

APPLICANT: ARGANI, PEDRAM

APPLICANT: ARGANI, PEDRAM

TATLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES

TITLE OF INVENTION: BANCREATIC CANCER DIAGNOSIS AND THERAPIES

TITLE OF INVENTION: BANCREATIC CANCER DIAGNOSIS AND THERAPIES

CURRENT FILING DATE: 2003-10-11

PRIOR PELLING DATE: 2001-10-11

PRIOR FILING DATE: 2001-10-11

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PARCELLIN VET: 2.1
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Pred. No. 4e-252;
0; Mismatches 15; Indels 0
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US-10-269-909-85
Sequence 85, Application US/10269909
Publication No. US20030180747A1
GENERAL INFORMATION:
                                                                                                                                                       CTTGCAAAAAAAAAAAA
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98.5%;
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Best Local Similarity 98.5
Matches 965, Conservative
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US-10-269-909-85
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RESULT 12
US-10-241-220-45
is Sequence 45, Application US/10241220
is Publication No. US20030148408A1
is GENERAL INFORMATION:
is APPLICANT: Frantz Gretchen
is APPLICANT: Phillips, Heidi
is APPLICANT: Phillips, Heidi
is APPLICANT: Phillips, Paul
is APPLICANT: Someor, Susan
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is APPLICANT: Williams, P. Mickey
is TITLE OF INVENTION: COMPOSITIONS AND
is TITLE OF INVENTION: TREATMENT OF TUMOR
is FILE REFERENCE: PSOIORI-US
is CURRENT PAPLICATION NUMBER: US/10/241,220
is CURRENT FILING DATE: 2002-12-13
is NUMBER OF SEQ ID NOS: 120
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AGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAAACAGAAAGGACACCCTCTCTAGGG
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                                                          CAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGGGGCGCATGGAGGGGCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1. Application US/09934249; Patent No. US20020115081A1.
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: CHENCHION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIONASCULAR CONDITIONS
TILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: LANCTH: 1321
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Best Local Similarity 98.3%;
Matches 809; Conservative
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US-09-934-249-1
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ORGANISM: Homo Sapiens
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                                      Query Match 74.9%; Score 795.2; DB 13
Best Local Similarity 99.6%; Pred. No. 3.5e-208;
Matches 797; Conservative 0; Mismatches 3;
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TYPE: DNA
CORGANISM: Homo Sapien
US-10-241-220-45
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Sequence 2, Application US/10390045 Publication No. US2030170713A1 GENERAL INFORMATION: APPLICANT: SELVASTAVA, SHIV

RESULT 13 US-10-390-045-2 ; Sequence 2, App. ; Publication No. ; GENERAL INFORMA; ; APPLICANT: SEL

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APPLICANT: MOUL, JUDD W.

APPLICANT: XU, LINDA M.

APPLICANT: XU, LINDA M.

APPLICANT: XU, LINDA M.

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

FILE REFERENCE: 04995.0057-00000

CURRENT APPLICATION NUMBER: US/10/390,045

PRIOR APPLICATION NUMBER: US/09/769,482

PRIOR APPLICATION NUMBER: US/09/769,482

PRIOR PELING DATE: 2001-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SEQ ID NOS: 67

SEG ID NOS: 67
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Pred. No. 8.1e-198;
0; Mismatches 1;
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99.9%;
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Best Local Similarity 99.9'
Matches 758; Conservative
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-10-390-045-2
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Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lendachulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
ITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
ITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
ITLE OF INVENTION: CARDIOWASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT FILLING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR PILLING DATE: 2000-08-22
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: FASTER OF SEQ for Windows Version 3.0 TYPE: DNA ORGANISM: Homo Sapiens FEATURE: NAME/KEY: CDS LOCATION: (1)...(861) US-09-934-249-3 US-09-934-249-3 LENGTH: 861 Query Match Best Local S Matches 761 567 142 202 262 267 322 327 382 387 442 447 507 562 502 ઠે g 셤 ઠે 셤 g a ద 셤 ò g ઠે ઠે ò ઠે ઠે ઠે 셤 ò

; TYPE: DNA ; ORGANISM: Homo sapien US-10-000-256A-32

Sequence 32, Application US/10000256A
| Publication No. US20030039983A1
| GENERAL INFORMATION:
| APPLICANT: Sun, Yongming
| APPLICANT: Recipon, Herve
| APPLICANT: Chen, Sei-Yu
| APPLICANT: Liu, Chenghua
| TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
| TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
| TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
| TITLE OF INVENTION NUMBER: US/10/000,256A
| TITLE OF INVENTION NUMBER: US/10/000,256A
| CURRENT APPLICATION NUMBER: 60/244,782
| PRIOR FILING DATE: 2000-11-01
| NUMBER OF SEQ ID NOS: 240
| SEQ ID NOS: 240
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| SEQ ID NOS: 240
| SEQ ID NOS: 240
| SEQ ID NOS: 240
| SEQ ID NOS: 240
| SEQ ID NOS: 240
| SEQ ID NOS: 240 681 686 741 746 801 806 GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAG AGAGAGCGCAGCCATCTGGAGCAAAGAGATAAACAGAAAGGACACCCTCTC 856 RESULT 15 US-10-000-256A-32 682 687 742 802 807 622 g ઠે g ò 셤 ò g ò

1004 1064 1124 430 944 490 670 550 610 825 GCGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCTTCGCC 885 CAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACCACGAGATCGAC 945 CTGCCACCCACCTATCTCGCTGTCAGAGGAGGAGGGCCCCCACCTACCAGGGCCCCCTGC 1005 ACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCA 1065 CCCCCAAACCAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGCCC 1125 TGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCGTG 371 CAGCGGGAGCGCTTCCACCCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGAC 431 CTGCCGCCCACCATCTCGCTGTCAGACGGGAAGGAGCCCCCCACCCTACCAGGGCCCCTGC 611 TGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCATG 311 GAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCTTTCGCC 491 ACCTCCAGCTTCGGGACCCCGAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCA 551 CCCCCAAACAAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCC Gaps 68.7%; Score 728.8; DB 15; Length 1583; 98.9%; Pred. No. 6.8e-190; ive 0; Mismatches 7; Indels 1; Best Local Similarity 98.9 Matches 744; Conservative Query Match 유 g g ద g g ò ò ò ò ò ò ò

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970 CCCTCCCCCCCCCCCCCCTGTGTATAAATTTTACATGTGTGTCTGGTCTGAATGCAC 1029
1485 CCCTCCCCTCCCACCTGTGTATAAAATATTTACATGTGATGTCTGGTCTGAATGCAC 1544
                                                                            1425 CCGCGCTTCTTAGAAGAGAGTGAGGAGGAAGGCGGGGGGCGCACAATCGCATGCGTGTGG 1484
           911 CCGCGCTTCTTAGAAGAGGAGTGAGAAGGCGGGGGGGGCGCAGCAACGCAT-CGTGTGG 969
                                                                                                                                                                                                1030 AAGCTAAGAGCTTGCAAAAAAAAAAAA 1061
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Search completed: December 8, 2003, 04:18:49 Job time : 1274 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

December Run on:

4, 2003, 19:50:19; Search time 31 Seconds (without alignments) 1511.867 Million cell updates/sec

US-09-857-826B-17

Title: Perfect score:

1 MAELEFVQIIIIVVVMMVMV......PLESAAIWSKEKDKQKGHPL 252 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

684280 seqs, 185983659 residues

684280

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*
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3: /cgn2\_6/ptodata/2/pubpaa/USO6\_NEW\_PUB.pep:\*
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18: /cgn2\_6/ptodata/2/pubpaa/USO0\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/2/pubpaa/USO0\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 56, Appl	Sequence 100, App	Sequence 101, App	Sequence 209, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 413, App	Sequence 2, Appli	Sequence 120, App	Sequence 11, Appl	Sequence 13, Appl	Sequence 58, Appl	Sequence 158, App	Sequence 12, Appl	Sequence 1836, Ap
SUMMAKIES	ΔID	US-09-796-753-56	US-10-241-220-100	US-10-241-220-101	US-10-301-822-209	US-09-821-812-3	US-10-390-045-3	US-10-205-823-413	US-09-934-249-2	US-10-241-220-120	US-10-390-045-11	US-09-934-249-13	US-09-796-753-58	US-10-000-256A-158	US-10-390-045-12	US-10-094-749-1836
		11	12	12	12	12	12	15	10	12	12	30	11	15	12	12
	Query Match Length DB	252	252	252	252	252	252	252	287	287	249	274	217	241	244	269
d	Query Match Leng	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.4	99.4	98.8	87.0	79.1	79.0	62.7	62.7
	Score	1348	1348	1348	1348	1348	1348	1348	1340	1340	1332	1172.5	1066.5	1063.5	845.5	845.5
	Result No.	<u></u>	ŀ,	М	4	S	9	7	80	0	10	4	(12	F	14	15

Sequence 0, Appli	ò	134	57	13	6	.6	14(	14	23	'n	Sequence 22, Appl	27	27.	14	1	œ	15	348	20,	27	324	333	63,	63,	331,	61,	61,	Sequence 14, Appl	4553
US-10-251-598-3	-10-251-59	US-09-870-759-134	8-60-	US-09-751-708A-134	US-10-200-562-197	-10-237-5	US-09-870-759-140	0	-10-	US-10-086-464-5	US-09-789-054A-22	.0-050-704-2	-10-	-6(	US-09-974-298-110	-10-288-79	9	-	US-10-192-381-20	US-09-919-039-278	US-10-153-668-324	-09-759-13	-10-188-49	10-1	-09-759-13	-10-188-49	-10-189-12	-10	US-10-060-036-4553
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306	288	830	830	830	1318	1318	830	830	2440	721	312	427	483	671	263	2429	527	527	366	707	859	649	649	649	671	671	671	876	876
62.5	58.7	7.7	7.7	7.7	7.6	9.6	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
842.5	791.5	104	104	104	103	103	100	100	100	99.5	66	66	66.	66	96	98		6	9	95.5	'n.	95	92	92	92	92	95	95	92
16			19					24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

## APPLICANT: MCCATTHY, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-99

CURRENT APPLICATION NUMBER: US/9/196,753

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR PILING DATE: 1998-10-30

PRIOR PILING DATE: 1998-10-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1999-02-26

PRIOR PILING DATE: 1999-03-01

PRIOR PILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-05-14

PRIOR PILING DATE: 1999-06-19

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-30

PRIOR PILING DATE: 1999-06-30

PRIOR PILING DATE: 1999-09-20

PRIOR PILING DATE: 1999-09-20

PRIOR PILING DATE: 1999-09-20

PRIOR PILING DATE: 1999-09-20

PRIOR PILING DATE: 1999-09-30

PRIOR PILING DATE: 1999-09-20

PRIOR PILING DATE: 1999-09-30

 Sequence 56, Application US/09796753; Publication No. US20030027998A1; GENERAL INFORMATION:

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; Sequence 101, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION;
CURRENT FILING DATE: 2002-12-13 UNDBER OF SEQ ID NOS: 120 ENG ID NO 100 LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spencer, Susan
Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu'lliams, P. Mickey
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SKEKDKQKGHPL 252
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Matches 252; Conservative
                                                                                                     TYPE: PRT
CORGANISM: Homo Sapien
US-10-241-220-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-241-220-101
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             PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR PRIOR PRILING DATE: 2000-05-14
PRIOR PRIOR DATE: 2000-05-14
PRIOR PRIOR DATE: 2000-05-19
PRIOR FILING DATE: 2000-06-19
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PRIOR PRIOR DATE: 2000-06-19
PRIOR PRILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,66
PRIOR PRILING DATE: 2000-09-20
PRIOR PRILING DATE: 2000-09-20
PRIOR PRILING DATE: 2000-09-20
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NUMBER OF SEQ ID NOS: 162
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Sublication No. US20030148408A1
GENERAL INPORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
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US-09-796-753-56
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US-10-241-220-100
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                                                                                                                  1 MAELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPS
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS OF TUMOR
FILE REFERENCE: P5010R1-US
FULE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
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Length 252;
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100.0%; Score 1348; DB 12;
100.0%; Pred. No. 9.4e-111;
tive 0; Mismatches 0;
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LENGTH: 252
TYPE: PRT
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS; AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                 181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHLAPLESAAIW 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1348; DB 12;
Pred. No. 9.4e-111;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     TILE REFERENCE: MPMO1-079PZNIM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002/11-21
PRIOR PRILING DATE: 2002/11-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PRILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PSECSEE Windows Version 4.0
SEQ ID NO 209
LENGTH: 252
                                                                                                                                                             Sequence 209, Application US/10301822
Publication NG. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Miltennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                        Berger, Allison
Guillemette, Tracy L.
Kamatkar, Shubhangi
Schlegel, Robert
Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/09821812; Publication No. US20030166520A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Some Similarity 100.0%; Powatches 252; Conservative 0;
                                                                                                                                                                                                                                                                                                  Thibodeau, Stephen N. Burgart, Lawrence J.
                                                                          241 SKEKDKQKGHPL 252
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                                                         241 SKEKDKOKGHPL 252
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; ORGANISM: Homo Sapiens
US-10-301-822-209
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APPLICANT:
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PPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 120
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Sequence 3, Application US/10390045

Sequence 3, Application US/10390045

Publication No. US20030170713A1

GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: MOUL, JUDD W.

APPLICANT: SEGAWA, TAKEHIKO

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

CURRENT APPLICATION NUMBER: US/10/390,045

CURRENT APPLICATION NUMBER: 2003-03-18
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                                                                                                                                                                                                                                                                                                                                                 Score 1348; DB 12; Length 252; Pred. No. 9.4e-111;
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APPLICANT: Lin Biaoyang
TITLE OF INVENTAON: Androgen Regulated Prostate Specific
TITLE OF INVENTAON: Nucleic Acids
FILE REFERENCE: k-IS 4373
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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NUMBER: US/10/390,045
$003-03-18
MNBER: US/09/769,482
2001-01-26
MNBER: GO/178,772
                                                                                            CURRENT APPLICATION NUMBER: US/09/821,812
CURRENT FILING DAME: 2001-03-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQ
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PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/176
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 00/175
PRIOR APPLICATION NUMBER: 00/175
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PARENTIN VEY: 2.1
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Best Local Similarity 100.0
Matches 252; Conservative
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Best Local Similarity 100.
Matches 252; Conservative
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ORGANISM: Homo sapiens
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US-09-821-812-3
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RESULT 9
US-10-241-220-120
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US-09-934-249-2
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERARY OF PROSITIE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2001-07-25
FRIOR APPLICATION NUMBER: 60/307,982
FRIOR APPLICATION NUMBER: 60/314,356
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: 60/341,746
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: 60/341,746
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: 60/341,746
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: 60/341,746
FRIOR FILING DATE: 2002-03-05
FRIOR FILING DATE: 2002-03-05
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                                                              61 ESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG 120
                                                                                                           121 EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180
                                                                                                                              181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
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                                   61 ESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAELEFVQIIIIVVVVMVVVVITCLLSHYKLSARSFISRHSQGRREDALSSEGCLWPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 413
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                             Sequence 413, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monahan, John E.
Endege, Wilson O.
Gannavarapu, Manjula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorbatcheva, Bella
Hoersch, Sebastianh
Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Xumei
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Best Local Similarity 100.
Matches 252; Conservative
                                                                                                                                                                                                                                                                                        241 SKEKDKOKGHPL 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-205-823-413
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APPLICANT:
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121 EEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGIS 180
                                                  181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                   181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSPQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
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Pred. No. 5.6e-110;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Landschulz, Katherine T.
APPLICANT: Tuxi, Thomas G.
APPLICANT: Tuxi, Thomas G.
APPLICANT: Thompson, John F.
TITLE OP INVENTION; DIAGNOSIS AND TREATMENT OF
TITLE OP INVENTION; DIAGNOSIS AND TREATMENT OF
TITLE OP INVENTION; DIAGNOSIS AND TREATMENT OF
TITLE OP INVENTION; CARDIOVASCULAR CONDITIONS
FILE REFERENCE: POŶ38/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2000/408-22
PRIOR FILING DATE: 2000/408-22
MINDER FILING DATE: 2000/408-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ows Version 3.0
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Phillips, Heidi
Polakis, Paul
Spencer, Susan
Williams, P. Mickey
Wu, Thomas
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APPLICANT: Hillan, Kenneth J
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Milliams, P. Micke
APPLICANT: Williams, P. Micke
                                                                                                                                                                                        SKEKDKQKGHPL 252
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Best Local Similarity 99.2
Matches 250; Conservative
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SOFTWARE: FastSEQ for Wind
SEQ ID NO 2
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US-09-934-249-2
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Publication No. US20030170713A1

GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: MUUL, JUDD W.

APPLICANT: XU, LINDA L.

APPLICANT: SCORMA, TAKEHIKO

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

FILE REFERENCE: 2003-0057-00000

CURRENT PAPLICATION NUMBER: US/10/399,045

CURRENT FILING DATE: 2001-01-26

PRIOR FILING DATE: 2000-01-28

SPIOR FILING DATE: 2000-01-28

SOFTWARE PRIOR PULING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE PATENTIN UNIVER: 21
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                            FOR THE DIAGNOSIS AND
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                                                                                                                                                                                                                                                                         Query Match 99.4%; Score 1340; DB 12; Length 287; Best Local Similarity 99.2%; Pred. No. 5.6e-110; Matches 250; Conservative 1; Mismatches 1; Indels 0
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS I
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REPRENCE: PSO10R1-03
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ 1D NOS: 120
LENGTH: 287
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ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
US-10-241-220-120
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US-10-390-045-11
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EPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISA 180
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   121
                             STVSGNGIPEPQVYAPPRPIDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGE 120
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Patent No. US20020115081A1

GENERAL INFORMATION:

APPLICANT: Lee, Richard T.

APPLICANT: Lendschulz, Katherine T.

APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS

FILE REFERENCE: P0738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT PAPLICATION NUMBER: US/09/934,249

CURRENT PAPLICATION NUMBER: US 60/227,159
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US-09-796-753-58
September 58, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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NKEKEKQKGHPL 274
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; ORGANISM: Mus Musculus
US-09-934-249-13
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US-10-000-256A-158
Sequence 158, Application US/10000256A
PUBLICANT: Sun, Youganing
APPLICANT: Sun, Youganing
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR FILING DATE: 2000-11-01
60 PPFIQRS---REQPTYPYLQHEIALPPTISLSDGEEPPPYOGPCTLQLRDPEQQLEINRE 116
                                                                                                                       61 QVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTL 120
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US-10-390-045-12
Squence 12, Application US/10390045
Squence 12, Application US/10390045
Publication No. US20030170713A1
GENRRAL INFORMATION:
APPLICANT: MOUL, JUDD W.
APPLICANT: WOLL, JUDD W.
APPLICANT: WOLL, JUDD W.
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
CURRENT APPLICATION NUMBER: US/10/390,045
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US/09/769,482
PRIOR APPLICATION NUMBER: 60/178,772
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                                                                                      147 SVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 QVYAPPRETDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPYQGPCTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Gaps
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Pred. No. 6.6e-86;
0; Mismatches 0; Indels 41;
                                                                                                                                                                                                                                  177 SSFQHQQSNGPSSLLEGTRLHHSHIAPLE----NKEKEKQKGHPL 217
                                                                                                                                                                                                    207 SSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL 252
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82.9%;
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Best Local Similarity 82.9
Matches 199; Conservative
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SOFTWARE: Patentin version
SEQ ID NO 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-10-000-256A-158
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  McCarthy, Sean A.
FINTION: SECRETED PROTEINS AND USES THEREOF
                                         TILLE OF LAUGHAILON: DELCALLE FORCER:
FILLE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR PELING DATE: 1998-10-30
PRIOR PELING DATE: 1998-12-30
PRIOR PELING DATE: 1999-12-30
PRIOR PELING DATE: 1999-12-30
PRIOR PELING DATE: 1999-02-26
PRIOR PELING DATE: 1999-03-01
PRIOR PELING DATE: 1999-03-01
PRIOR PELING DATE: 1999-03-01
PRIOR PELING DATE: 1999-06-19
PRIOR PELING DATE: 1999-06-19
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PRIOR PELING D
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PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
LENGTH: 217
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Best Local Similarity, 88.9%;
Matches 201; Conservative
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; ORGANISM: Mouse
US-09-796-753-58
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Search completed: December 4, 2003, 19:53:23
Job time : 32 secs
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                                                                                                                                                                                                                                                                                            2 AELEFVQIIIIVVVVMVVVVITCLLSHYKLSARSFISRHSOGRRREDALSSEGCLWPSE
                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                  DB 12; Length 244;
                                                                                                                                                                                                                Query Match 62.7%; Score 845.5; DB 12; Length Best Local Similarity 67.6%; Pred. No. 1.6e-66; Matches 169; Conservative 21; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: NAGAI, KEIICHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
FRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver: 2.1
SENGTH: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1836, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 12
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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235 IKGKDRKPGN 244
                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT ORGANISM: Homo sapiens

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US-10-094-749-1836
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141
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                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 ASTCSSNGRWEGPPPTYSEVMGHHPGASFLHHQRS---NAHRGSRLQFQQ-NNAESTIVP 257
                                                                                                                                                                                                                   62 STVSGNGIPEPQVYAPPRPIDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPPTISLSDGE 121
                                                                                                               61
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                                                                                                         2 AELEFVQIIIIVVVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSE
                                                                                                                                           24 AELEFAQIIIIVVVVTVMVVVIVCLLMHYKVSTRSFINRPNQSRRREDGLPQEGCLWPSD
                                                                                                                                                                                                                                                  84 SAAPRLGASE--IMHAPRSRDRFTAPSFIQRDRFSRFQPTYPYVQHEIDLPPTISLSDGE
                                                          Gaps
                                                          ..
     DB 12; Length 269;
                                                          53; Indels
62.7%; Score 845.5; DB 1;
67.6%; Pred. No. 1.8e-66;
tive 21; Mismatches 53
Query Match
Best Local Similarity 67.6%
Matches 169; Conservative
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258 IKGKDRKPGN 267
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

December 8, 2003, 04:18:58; Search time 387 Seconds (without alignments) 9111.986 Million cell updates/sec Run on:

US-09-857-826B-44 Title: Perfect score:

Sequence:

Scoring table:

OLIGO\_NUC Gapop\_60.0 , Gapext 60.0

2201672 seqs, 1661799599 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Published Published Database :

cgn2\_6/ptodate3/2/pubpna/USO7 PUBCOMB.seq:\*
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/cgn2\_6/ptodate3/2/pubpna/USO9\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

					COTACATAC	
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Result		Query				
No.	Score	Match	Match Length DB	8	aı	Description
~	961	9.06	696	17	US-09-796-753-55	Sequence 55, Appl
7	926	87.3	1141	13	US-10-301-822-208	208
e	926	87.3	1141	15	US-10-205-823-412	Sequence 412, App
4	926	87.3	1850	13	US-10-241-220-44	
S	926	87.3	4527	13	US-09-821-812-2	Sequence 2. Appli
9	912	86.0	1140	13	US-10-390-045-1	4
7	902	85.0	4839	13	US-10-241-220-119	Sequence 119, App
60	902	85.0	4839	13	US-10-269-909-84	84,
6	902	85.0	4839	13	US-10-269-909-85	85,
10	891	84.0	1066	14	US-10-098-841-71	Sequence 71, Appl
11	788	74.3	908	13	US-10-241-220-45	45
12	749	70.6	1321	10	US-09-934-249-1	-
13	708	66.7	759	13	US-10-390-045-2	Sequence 2, Appli
14	701	66.1	861	20	US-09-934-249-3	٠.,
15	509	48.0	1583	15	US-10-000-256A-32	٠.,

	Sequence 20/4, Ap			Sequence 12, App	Seguence 57, Appl	Sequence 20542, A	Sequence 3776, Ap	Sequence 3936, Ap	Sequence 20699, A	Sequence 15, App	Sequence 16, App	Sequence 25133,			Sequence 1705		Sequence 3121	Sequence 1990				Sequence 5, Appli					Sequence 371	Sequence 62, Appl
US-U9-934-249-14	US-US-918-935-20/4 IIS-09-783-590-3464	US-09-908-975-13620	US-09-783-590-3488	US-09-934-249-12	US-09-796-753-57	US-09-864-761-20542	US-09-864-761-3776	US-09-864-761-3936	US-09-864-761-20699	US-09-934-249-15	US-10-293-582-16	US-10-029-386-25133	US-09-860-670-159	US-09-738-885-3	US-09-864-761-17053	US-09-864-761-230	US-09-864-761-3121	US-09-864-761-19900	US-10-029-386-22252	US-10-029-386-9045	US-10-029-386-20432	US-10-390-045-5	US-10-390-045-6	US-10-390-045-10	US-10-106-698-3514	US-10-005-169-6	US-10-029-386-3710	US-09-853-386-62
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313	103	9	20	44	44	32	32	29	29	. 59	29	26	26	56	25	25	25	25	25	25	25	24	24	24	24	24	24	24
16	- 6	13	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Sequence 55, Application US/09796753 Publication No. US20030027998A1 GENERAL INFORMATION

APPLICANT: McCarthy, Sean A. TITLE OF INVENTION: SECRETE PROTEINS AND USES THEREOF FILE REPERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US/183,175
PRIOR PILING DATE: 1998-10-30

APPLICATION NUMBER: FILING DATE: 1998-

OR APPLICATION NUMBER: 09/223,546
OR FILING DATE: 1998-12-30
OR APPLICATION NUMBER: 09/224,246
OR FILING DATE: 1998-12-30
OR APPLICATION NUMBER: 09/259,388
OR FILING DATE: 1999-02-26
OR APPLICATION NUMBER: 0/122,458
OR FILING DATE: 1999-03-01
OR APPLICATION NUMBER: 09/312,359
OR FILING DATE: 1999-03-14 1998-12-30 1999-06-18 APPLICATION NUMBER: FILING DATE: PRANCA PR

1999-06-30 1999-07-30 1999-09-20 1999-06-2 APPLICATION NUMBER: FILING DATE: 1999-CAPPLICATION NUMBER:

APPLICATION NUMBER: 09/471,179 FILING DATE: 1999-12-23 1999-09-30

Page

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Best Local Similarity 99.5
Matches 976; Conservative
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90.6%; Score 961; DB 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 961; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 09/514,010
PRIOR PILING DATE: 2000-02-25
PRIOR PILING DATE: 2000-02-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
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PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
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; NAME/KEY: CDS
; LOCATION: (6)...(761)
US-09-796-753-55
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LENGTH: 969
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Shubhangi
APPLICANT: Guillemette, Shubhangi
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Marchos For IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: MOTHOS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: METHOS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERARY OF COLON CANCER
TITLE REFERENCE: MPMOI-029PZRNM
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-01-05
PRIOR FILING DATE: 2002-03-05
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Pred. No. 0;
0; Mismatches
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CACGETCETTCATCACCGGCACACAGCCAGGGGGGGAGAGAAAAATGCCCTGTCCTCAG
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                                 TGGTGATGATGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTG
                                                                 TCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGC
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RESULT 3 US-10-205-823-412 ; Sequence 412, Application US/10205823

APPLICANT: Schizel, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersch, Sebastian
APPLICANT: Hoersch, Sebastian
APPLICANT: Mansey, Angela M.
APPLICANT: Mansey, Angela M.
APPLICANT: Mansey, Angela M.
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Mansey, METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF PROSTATE CANCER
APPLICANT: MILON HORBER: 60/307,982
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: MUMBER: 60/307,982
RICHERING DATE: 2001-07-25
PRIOR FILING DATE: 2001-09-25
PRIOR PLICATION NUMBER: 60/314,356
PRIOR PLILING DATE: 2001-09-25
PRIOR PLILING DATE: 2001-10-12-12
PRIOR PLILING DATE: 2001-12-12
PRIOR PLILING DATE: 2001-12-12
PRIOR PLILING DATE: 2001-12-12
PRIOR PLILING DATE: 2001-12-12
PRIOR PLILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SSETUD NO 412 GTCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGG 135 200 TGGTGATGGTGATGGTGGTGGTGGTGATCACGTGCTGCTGAGCCACTACAAGCTGTCTG 195 260 255 AAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGG 320 AAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGG 315 440 435 500 495 CCATCTCGCTGTCAGACGGGGAGCCCCCACCTACAGGGCCCCTGCACCGCCCCTCCAGC ! CACGGTCCTTCATCAGCCGGCACAGCCGGGGGGGGGGGAGAGATGCCCTGTCCTCAG CACGGTCCTTCATCAGCCGCACAGCCAGGGCGGAGAGAAGAAGATGCCCTGTCCTCAG TGGTGATGATGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTG GCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCA GCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCCA GTCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATGGTGG Gaps . Length 1141; Indels DB 15; Score 926; DB Pred. No. 0; 0; Mismatches 87.3%; 99.9%; APPLICANT: Schlegel, Robert APPLICANT: Monahan, John E. APPLICANT: Endege, Wilson O. Query Match 87.3 Best Local Similarity 99.9 Matches 976; Conservative ORGANISM: Homo sapiens US-10-205-823-412 94 141 136 201 196 261 316 376 441 81 256 321 381 436 501 496 TYPE: DNA ò g

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Publication No. US2030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Phillips, Heidi
APPLICANT: Phillips, Heidi
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APPLICANT: Phillips, Heidi
APPLICANT: Williams, Poner, Susan
APPLICANT: Williams, P. Mickey
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ORGANISM: Homo Sapien
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LENGTH: 1850
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Sequence 2, Application US/09821812
Publication No. US20030166520A1
GENERAL INFORMATION:
TATLE OF INVENTION: Androgen Regulated Prostate Sperific OF INVENTION: Nucleic Acids
TITLE OF INVENTION: Nucleic Acids
FILE REFERENCE: P-IS 4373
CURRENT APPLICATION NUMBER: US/09/821,812
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Sequence 1, Application US/10390045
; Bublication No. US20030170713A1
; GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, UUDD W.
APPLICANT: MOUL, UUDD W.
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POSTATE: 20057-00000
CURRENT APPLICATION NUMBER: US/10/390,045
CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-38
; PRIOR FILING DATE: 2000-01-38
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
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ive 0; Mismatches
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Best Local Similarity 99.9
Matches 962; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (95)..(850)
US-10-390-045-1
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                                                                                                                                                               DB 13; Length 4527;
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                                                                                                                                                             Score 926; I
Pred. No. 0;
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                          Query Match
Best Local Similarity 99.9%;
Matches 976; Conservative
                           SEQ ID NO 2
LENGTH: 4527
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(851)
US-09-821-812-2
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                                                                                                                       ATCAGCGCCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCCCACCTACAGC
                                                                                                                                                                                 GAGGTCATCGGCCACTACCCGGGGTCCTCCTACCAGCACCAGCAGCAGTGGCCCC
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                                                                                                       ATCAGCGCCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGC
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APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Tanan, Samin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF TUMOR
TITLE OF INVENTION OF TUMOR
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
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llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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Sequence 119, Application US/10241220
Publication No. US20030148408A1
GENERAL INFRMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapien
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Best Local Similarity
Matches 952; Conserv
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Sequence 84, Application US/10269909

Sequence 84. Application US/1026909

Publication No. US20030180747A1

GENERAL INFORMATION:

APPLICANT: HRUBAN, RALPH H.

APPLICANT: ARGANI, PEDRAM

APPLICANT: ARGONIC-DONAHUE, CHRISTINE

APPLICANT: MAITRA, ANIRBAN

TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
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US-10-269-909-85

US-10-269-909-85

Sequence 85, Application US/10269909

Publication No. US20830180747A1

GENERAL INFORMATION:
APPLICANT: HRUBAN, RALPH H.
APPLICANT: ARGANI, PEDRAM
APPLICANT: MACOBUZIO-DONAHUE, CHRISTINE
APPLICANT: MACOBUZIO-DONAHUE, CHRISTINE
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
FILE REFERENCE: 58303 (7169)
CURRENT APPLICATION NUMBER: US/10/269,909
CURRENT FILING DATE: 2003-10-11
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-11-11
SRIOR APPLICATION NUMBER: 60/328,609

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 87

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Pred. No. 0;
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FILE REFERENCE: 58303 (71699)
CURRENT APPLICATION NUMBER: US/10/269,909
CURRENT FILING DATE: 2003-10-11
PRIOR APPLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: 4839
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Best Local Similarity 99.9
Matches 952; Conservative
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CRGANISM: Homo sapiens
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APPLICANT: Drmanac, Radoje J.
TITLE OF INVENTION: No. U520020197679Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2
CURRENT APPLICATION NUMBER: U5/10/098,841
CURRENT APPLICATION NUMBER: 09/598,042
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ 1D NOS: 331
SEQ ID NO 71
LENGTH: 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71, Application US/10098841
Publication No US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Tang, Ping
APPLICANT: Tang, Ping
APPLICANT: Chen, Rui, ApplicANT: Chen, Rui, hong
APPLICANT: Ren, Feiyan
APPLICANT: Ghen, Rui, hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Weny, Chiwei
APPLICANT: Weny, Chiwei
APPLICANT: Weny, Chiwei
APPLICANT: Weny, Dunrui
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Qian, Xiaohong B.
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                                                    TTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGGTGATCACCTGCC
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                                        TTGTTCAGATCATCATCATCGTGGTGGTGATGGTGATGGTGGTGGTGGTGATCACGTGCC
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                    ó,
Score 891; DB 14; Length 1066;
Pred. No. 0;
0; Mismatches 1; Indels 0
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99.9%;
Query Match
Best Local Similarity 99.9
Matches 941; Conservative
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RESULT 11 US-10-241-220-45

FEATURE: NAME/KEY: CDS LOCATION: /154 σ

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AACTGAACCGGGGGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 584
                                                        GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG
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   TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
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                                      TAGAGAGCGCAGCCATCTGGAGCAAAGAGGATAAACAGAAAGGACACCCTCTCTAGG
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                    Sequence 1, Application US/09934249;
Sequence 1, Application US/09934249;
Ratent No. US20020115081A1;
GENERAL INFORMATION:
APPLICANT: Leadschulz, Katherine T.
APPLICANT: Thompson, John F.
APPLICANT: TOWN NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (413)...(1273)
US-09-934-249-1
                                                                                                                               TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                           GICCCCAG 868
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US-09-934-249-1
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                                             SUBLEACH IN FURLILLY.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Palalis, Palal

APPLICANT: Polakis, Paul

APPLICANT: Spencer, Susan

APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TITLE OF INVENTION: TREATMENT OF TUMOR

FILE REFERENCE: PSOLORI-US

CURRENT APPLICATION NUMBER: US/10/241,220

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Sequence 45, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
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Patent No. US20020115081A1

GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thrompson, John F.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: DATE: 2001-08-21

PRIOR PILLING DATE: 2001-08-21

PRIOR PILLING DATE: 2000-08-21

PRIOR PILLING DATE: 2000-08-21

WUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 751; Conservative (
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ORGANISM: Homo Sapiens
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; LOCATION: (1)...(861)
US-09-934-249-3
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; Publication No. US20030170713A1
; GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057 00000
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057 00000
; CURRENT APPLICATION NUMBER: US/10/390,045
CURRENT PILING DATE: 2003-03-18
; PRIOR PILING DATE: 2000-01-28
; PRIOR PPLICATION NUMBER: 60/178,772
; PRIOR PPLICATION NUMBER: 60/179,72
; PRIOR PPLING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 759
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Best Local Similarity 99.9%;
Matches 758; Conservative
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Score 509; DB 15; Pred. No. 6.3e-228; 0; Mismatches 1;

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Query Match
Best Local Similarity 99.8
Matches 559; Conservative
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Publication No. US2003003983A1

GENERAL INFORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX.0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2000-11-01
FRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 240
SOFTHARE: Patentin version 3.1
SEQ ID NO 32
LEGGTH: 1583
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